

From: Chan, Christina
 Sent: Wednesday, January 26, 2005 2:45 PM
 To: Ramirez, Delia; STIC-Biotech/ChemLib
 Subject: RE: rush search 09/886400

Please rush. Thanks Chris

CRPE

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
 (571)-272-0841
 Remsen, 3E89

-----Original Message-----

From: Ramirez, Delia
 Sent: Wednesday, January 26, 2005 2:39 PM
 To: Chan, Christina
 Subject: rush search 09/886400

Hi Christina,

Please approve the following interference search: SEQ ID NO: 4 in the protein and nucleic acid databases

Thank you very much,

Delia M. Ramirez, Ph.D.
 Patent Examiner
 Recombinant Enzymes-Art Unit 1652
 USPTO
 400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
 Alexandria, VA 22314
 (571) 272-0938
 delia.ramirez@uspto.gov

STAFF USE ONLY

Searcher: *Am*
 Searcher Phone: 2-2504
 Date Searcher Picked up: 1/27/05
 Date Completed: 2/1/05
 Searcher Prep/Rev. Time: 10
 Online Time: 15

Type of Search
 NA Sequence: #
 AA Sequence: #
 Structure: #
 Bibliographic:
 Litigation:
 Patent Family:
 Other:

Vendors and cost where applicable
 STN:
 DIALOG:
 QUESTEL/ORBIT:
 LEXIS/NEXIS:
 SEQUENCE SYSTEM:
 WWW/Internet:
 Other(Specify):

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 27, 2005, 05:58:26 ; Search time 62 Seconds

(without alignments) 2121.118 Million cell updates/sec

Title: US-09-886-400a-4

Perfect score: 1879

Sequence: 1 LRALVFGHGNLQYAEIPKSEI.....RRLDAFPRAIYNDWGRGNGEP 364

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep:*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	100.0	364	14	US-10-112-231A-4
2	99.5	364	9	US-09-886-000-4
3	99.5	364	13	US-10-112-357-4
4	99.5	364	13	US-10-114-403-4
5	99.5	364	13	US-10-116-606-4
6	99.5	364	13	US-10-112-331-4
7	99.5	364	13	US-10-112-377-4
8	99.5	364	13	US-10-116-581-4
9	99.5	364	13	US-10-112-442-4
10	99.5	364	13	US-10-112-418-4
11	99.5	364	13	US-10-114-083-4
12	5.9	364	15	US-10-282-122A-53281
13	5.8	312	14	US-10-369-493-23237

RESULT 1
US-10-112-231A-4
; Sequence 4, Application US/10112231A
; Publication No. US20030184276A1
; GENERAL INFORMATION:
; APPLICANT: Reid, John
; TITLE OF INVENTION: ALPHA GALACTOSIDASES AND METHODS FOR
; CURRENT APPLICATION NUMBER: MAKING AND USING THEM (Amended)
; CURRENT FILING DATE: 2003-03-29
; PRIORITY FILING DATE: 1999-09-20
; PRIORITY FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE ID: FastSEQ for Windows Version 4.0.
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Thermococcus alcaliphilus

US-10-112-231A-4
Query Match Score 100.0%; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 8.4e-165;
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RESULT 2
US-09-886-400-4
; Sequence 4, Application US/09886400
; Patent No. US2002004522A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: Murphy, Dennis
; APPLICANT: Ried, John
; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH
; FILE REFERENCE: DIVER1120-4
; CURRENT APPLICATION NUMBER: US/09/886, 400
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 09/613, 220
; PRIOR FILING DATE: 1996-03-08
; PRIOR APPLICATION NUMBER: 09/619, 032
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/407, 806
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/407, 806
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Thermococcus alcaliphilus
US-09-886-400-4

Query Match, Best Local Similarity 99.5%; Score 1870; DB 9; Length 364;
Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 LRALVFGHGMQYAETPKSIPKVKIEKAYIPVIETIKEIPRGLNTGYTLKFLRKD IID 60
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Db 181 LRELRAKAKLUVFEGKVTKAVKQDIEAVVWVAVNTAVALGICRLPLMNPKVASYWEDKD 240
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Db 241 NILLYGTDIEFIGYRDIGYRMSVEGLIEVDRINSELCLPSELKHSGRELYRTSSWAP 300
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Db 361 NGEP 364
QY 361 NGEP 364

RESULT 3
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; Sequence 4, Application US/10112357
; Publication No. US2002011509A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: Murphy, Dennis
; APPLICANT: Ried, John
; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH
; FILE REFERENCE: DIVER1120-4
; CURRENT APPLICATION NUMBER: US/10/112, 357
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/886, 400
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 09/619, 032
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/407, 806
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/613, 220
; PRIOR FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Thermococcus alcaliphilus
US-10-112-357-4

Query Match, Best Local Similarity 99.5%; Score 1870; DB 13; Length 364;
Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRALVFGHGNLQAEPKSEPKVKIEKAYIPVIETIKEIPRGLNTGYTLKFLRKD IID 60
Db 1 LRALVFGHGNLQAEPKSEPKVKIEKAYIPVIETIKEIPRGLNTGYTLKFLRKD IID 60
QY 61 LVKGIGASDLIBIGTSYTHAILPLPLSRVEAQVQRDRKEELFEVSKGFWPLAY 120
Db 61 LVKGIGASDLIBIGTSYTHAILPLPLSRVEAQVQRDRKEELFEVSKGFWPLAY 120
QY 121 DPPIPAIKDONGYELFADGEAMLSAHLNSAIPKIPLYPHIKAQREKFRYISLG 180
Db 121 DPPIPAIKDONGYELFADGEAMLSAHLNSAIPKIPLYPHIKAQREKFRYISLG 180
QY 181 LRELRAKAKLUVFEGKVTKAVKQDIEAVVWVAVNTAVALGICRLPLMNPKVASYWEDKD 240
Db 181 LRELRAKAKLUVFEGKVTKAVKQDIEAVVWVAVNTAVALGICRLPLMNPKVASYWEDKD 240
QY 241 NILLYGTDIEFIGYRDIGYRMSVEGLIEVDRINSELCLPSELKHSGRELYRTSSWAP 300
Db 241 NILLYGTDIEFIGYRDIGYRMSVEGLIEVDRINSELCLPSELKHSGRELYRTSSWAP 300
QY 301 DKSLRWRDEGENARLNMLSYNMRGELAFLAENSDARGWEPPLPERRDAFRAINYDWRGE 360
Db 301 DKSLRWRDEGENARLNMLSYNMRGELAFLAENSDARGWEPPLPERRDAFRAINYDWRGE 360
QY 361 NGEP 364
Db 361 NGEP 364

RESULT 4
US-10-114-403-4
; Sequence 4, Application US/10114403
; Publication No. US2002011100A1
; GENERAL INFORMATION:

||||| APPLICANT: DIVERSA CORPORATION
 ||||| APPLICANT: Murphy, Dennis
 ||||| TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND
 ||||| METHODS OF USE THEREOF
 ||||| FILE REFERENCE: DIVER1120-4
 ||||| CURRENT APPLICATION NUMBER: US/10/114,403
 ||||| PRIOR FILING DATE: 2002-04-01
 ||||| PRIOR APPLICATION NUMBER: 09/886,400
 ||||| PRIOR FILING DATE: 2001-06-20
 ||||| PRIOR APPLICATION NUMBER: 09/619,032
 ||||| PRIOR FILING DATE: 2000-07-19
 ||||| PRIOR APPLICATION NUMBER: 09/407,806
 ||||| PRIOR FILING DATE: 1999-09-20
 ||||| PRIOR APPLICATION NUMBER: 08/613,220
 ||||| PRIOR FILING DATE: 1996-03-08
 ||||| NUMBER OF SEQ ID NOS: 4
 ||||| SOFTWARE: FastSEQ for Windows Version 4.0
 ||||| SEQ ID NO: 4
 ||||| LENGTH: 364
 ||||| TYPE: PRT
 ||||| ORGANISM: Thermococcus alcaliphilus
 ; US-10-114-403-4

Query Match 99.5%; Score 1870; DB 13; Length 364;
 Best Local Similarity 99.5%; Pred. No. 5.7e-165; Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRALVPHGNQYAEIPKSEIPKVKAYKIVPIVETIJKKEIPFGLNNTGYTUKFLPKDID 60
 Db 1 LRALVPHGNQYAEIPKSEIPKVKAYKIVPIVETIJKKEIPFGLNNTGYTUKFLPKDID 60
 Qy 61 LVKGGSIASDLEIIGTSYTHAILPLPLSRVEAQVORDREVKEELFSPKGFWLPLAY 120
 Db 61 LVKGGSIASDLEIIGTSYTHAILPLPLSRVEAQVORDREVKEELFSPKGFWLPLAY 120
 Qy 61 LVKGGSIASDLEIIGTSYTHAILPLPLSRVEAQVORDREVKEELFSPKGFWLPLAY 120
 Db 61 LVKGGSIASDLEIIGTSYTHAILPLPLSRVEAQVORDREVKEELFSPKGFWLPLAY 120
 Qy 121 DP1PAIKONGYELFADGEAMFSAHNSAIKPKLYPHLKAQREKFRYISYLG 180
 Db 121 DP1PAIKONGYELFADGEAMFSAHNSAIKPKLYPHLKAQREKFRYISYLG 180
 Qy 121 DP1PAIKONGYELFADGEAMFSAHNSAIKPKLYPHLKAQREKFRYISYLG 180
 Db 121 DP1PAIKONGYELFADGEAMFSAHNSAIKPKLYPHLKAQREKFRYISYLG 180
 Qy 181 LRELRAIKUVFEGKVTLKAVKDIEAVPVWVAVNTAVMGLGRLPLMNPKVASHIEDKO 240
 Db 181 LRELRAIKUVFEGKVTLKAVKDIEAVPVWVAVNTAVMGLGRLPLMNPKVASHIEDKO 240
 Qy 241 NILYGTDFIPIGYRDIAIGRMSVGGLEVIDELNSELCLPSELKHSGRBLYRSTSWAP 300
 Db 241 NILYGTDFIPIGYRDIAIGRMSVGGLEVIDELNSELCLPSELKHSGRBLYRSTSWAP 300
 Qy 301 DKSURWREDEGNARLNMLSYNMRGELAFLAENSARGWPLPERRLDARAIYNDWRGE 360
 Db 301 DKSURWREDEGNARLNMLSYNMRGELAFLAENSARGWPLPERRLDARAIYNDWRGE 360
 Qy 361 NGEP 364
 Db 361 NGEP 364

RESULT 5
 US-10-116-606-4
 ; Sequence 4, Application US/10116606
 ; Publication No. US20020119515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: Murphy, Dennis
 ; APPLICANT: Ried, John
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH
 ; FILE REFERENCE: DIVER1120-4
 ; CURRENT APPLICATION NUMBER: US/10/112,331
 ; PRIOR FILING DATE: 2002-03-29
 ; PRIOR APPLICATION NUMBER: US/09/886,400
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 09/619,032
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/407,806
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 08/613,220
 ; PRIOR FILING DATE: 1996-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 4
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Thermococcus alcaliphilus
 ; US-10-112-331-4

Query Match 99.5%; Score 1870; DB 13; Length 364;
 Best Local Similarity 99.5%; Pred. No. 5.7e-165; Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRALVPHGNQYAEIPKSEIPKVKAYKIVPIVETIJKKEIPFGLNNTGYTUKFLPKDID 60
 Db 1 LRALVPHGNQYAEIPKSEIPKVKAYKIVPIVETIJKKEIPFGLNNTGYTUKFLPKDID 60
 Qy 181 LRELRAIKUVFEGKVTLKAVKDIEAVPVWVAVNTAVMGLGRLPLMNPKVASHIEDKO 240
 Db 181 LRELRAIKUVFEGKVTLKAVKDIEAVPVWVAVNTAVMGLGRLPLMNPKVASHIEDKO 240
 Qy 241 NILYGTDFIPIGYRDIAIGRMSVGGLEVIDELNSELCLPSELKHSGRBLYRSTSWAP 300
 Db 241 NILYGTDFIPIGYRDIAIGRMSVGGLEVIDELNSELCLPSELKHSGRBLYRSTSWAP 300
 Qy 301 DKSURWREDEGNARLNMLSYNMRGELAFLAENSARGWPLPERRLDARAIYNDWRGE 360
 Db 301 DKSURWREDEGNARLNMLSYNMRGELAFLAENSARGWPLPERRLDARAIYNDWRGE 360
 Qy 361 NGEP 364
 Db 361 NGEP 364

RESULT 6
 US-10-112-331-4
 ; Sequence 4, Application US/10112331
 ; Publication No. US20020119550A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: Murphy, Dennis
 ; APPLICANT: Ried, John
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH
 ; FILE REFERENCE: DIVER1120-4
 ; CURRENT APPLICATION NUMBER: US/10/112,331
 ; PRIOR FILING DATE: 2002-03-29
 ; PRIOR APPLICATION NUMBER: US/09/886,400
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 09/619,032
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/407,806
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 08/613,220
 ; PRIOR FILING DATE: 1996-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 4
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Thermococcus alcaliphilus
 ; US-10-112-331-4

RESULT 9

US-10-112-442-4

Sequence 4, Application US/10112442
Publication No. US20020150997A1
GENERAL INFORMATION:
APPLICANT: DIVERA CORPORATION
APPLICANT: Murphy, Dennis
APPLICANT: Murphy, Dennis
APPLICANT: Murphy, Dennis
TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: DIVER1120-4
CURRENT APPLICATION NUMBER: US/10/112,442
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 09/886,400
PRIOR FILING DATE: 2001-05-20
PRIOR APPLICATION NUMBER: 09/619,032
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/407,806
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 364
TYPE: PRT
ORGANISM: Thermococcus alcaliphilus
US-10-112-442-4

Query Match 99 %; Score 1870; DB 13; Length 364;
Best Local Similarity 99 %; Pred. No. 5.7e-165;
Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRALVFGHNLQYAEIPKSEPKVIEKAYVIETLKEIPFGLNITGYTLKFLPKDID 60
Db 1 LRALVFGHNLQYAEIPKSEPKVIEKAYVIETLKEIPFGLNITGYTLKFLPKDID 60
Qy 61 LVGGTASDIEIIGTSYTHAILPLPLSRVEAQVDRVKEELPEVSKGFWLPELAY 120
Db 61 LVGGTASDIEIIGTSYTHAILPLPLSRVEAQVDRVKEELPEVSKGFWLPELAY 120
Qy 121 DP1IPAIKONGYELFADGEMFLSAHNSAIKPKIPLKPHLTKAQRERFRYTSYLLG 180
Db 121 DP1IPAIKONGYELFADGEMFLSAHNSAIKPKIPLKPHLTKAQRERFRYTSYLLG 180
Qy 181 LRELRAIKLVFEGKVTLKAVKDTEAVPVWAVNTAVMLGIGRPLMNPKVSWIEDKO 240
Db 181 LRELRAIKLVFEGKVTLKAVKDTEAVPVWAVNTAVMLGIGRPLMNPKVSWIEDKO 240
Qy 241 NILYGTDEFIIGYRDIAGYRMSVGLLEVIDELNSCLPSELKSGEYLRTSSWAP 300
Db 241 NILYGTDEFIIGYRDIAGYRMSVGLLEVIDELNSCLPSELKSGEYLRTSSWAP 300
Qy 301 DKSLRIWREDEGNARLNMLSYNMRGELAFLAENSARGWBLPERRLDAPRATYNDWRGE 360
Db 301 DKSLRIWREDEGNARLNMLSYNMRGELAFLAENSARGWBLPERRLDAPRATYNDWRGE 360
Qy 361 NGEP 364
Db 361 NGEP 364

RESULT 10

US-10-112-418-4

Sequence 4, Application US/10114083
Publication No. US20020160464A1
GENERAL INFORMATION:
APPLICANT: DIVERA CORPORATION
APPLICANT: Murphy, Dennis
APPLICANT: Murphy, Dennis
APPLICANT: Murphy, Dennis
TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: DIVER1120-4
CURRENT APPLICATION NUMBER: US/10/112,418
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 09/886,400
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 09/619,032
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/407,806
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/613,220
PRIOR FILING DATE: 1996-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 364
TYPE: PRT
ORGANISM: Thermococcus alcaliphilus
US-10-112-418-4

Query Match 99 %; Score 1870; DB 13; Length 364;
Best Local Similarity 99 %; Pred. No. 5.7e-165;
Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRALVFGHNLQYAEIPKSEPKVIEKAYVIETLKEIPFGLNITGYTLKFLPKDID 60
Db 1 LRALVFGHNLQYAEIPKSEPKVIEKAYVIETLKEIPFGLNITGYTLKFLPKDID 60
Qy 61 LVGGTASDIEIIGTSYTHAILPLPLSRVEAQVDRVKEELPEVSKGFWLPELAY 120
Db 61 LVGGTASDIEIIGTSYTHAILPLPLSRVEAQVDRVKEELPEVSKGFWLPELAY 120
Qy 121 DP1IPAIKONGYELFADGEMFLSAHNSAIKPKIPLKPHLTKAQRERFRYTSYLLG 180
Db 121 DP1IPAIKONGYELFADGEMFLSAHNSAIKPKIPLKPHLTKAQRERFRYTSYLLG 180
Qy 181 LRELRAIKLVFEGKVTLKAVKDTEAVPVWAVNTAVMLGIGRPLMNPKVSWIEDKO 240
Db 181 LRELRAIKLVFEGKVTLKAVKDTEAVPVWAVNTAVMLGIGRPLMNPKVSWIEDKO 240
Qy 241 NILYGTDEFIIGYRDIAGYRMSVGLLEVIDELNSCLPSELKSGEYLRTSSWAP 300
Db 241 NILYGTDEFIIGYRDIAGYRMSVGLLEVIDELNSCLPSELKSGEYLRTSSWAP 300
Qy 301 DKSLRIWREDEGNARLNMLSYNMRGELAFLAENSARGWBLPERRLDAPRATYNDWRGE 360
Db 301 DKSLRIWREDEGNARLNMLSYNMRGELAFLAENSARGWBLPERRLDAPRATYNDWRGE 360
Qy 361 NGEP 364
Db 361 NGEP 364

RESULT 11

US-10-114-083-4

Sequence 4, Application US/10114083
Publication No. US20020160464A1
GENERAL INFORMATION:
APPLICANT: DIVERA CORPORATION
APPLICANT: Murphy, Dennis
APPLICANT: Murphy, Dennis
TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: DIVER1120-4
CURRENT APPLICATION NUMBER: US/10/114,083
CURRENT FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 09/886,400
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 09/619,032
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/407,806
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 08/613,220
; PRIOR FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Thermococcus alcaliphilus
; US-10-114-083-4

Query Match 99.5%; Score 1870; DB 13; Length 364;
Best local Similarity 99.5%; Pred. No. 5.7e-165; 1; Mismatches 362; Conservative 1; Indels 0; Gaps 0; Matches 362;

Qy 1 LRALYFHNQYAEIPKSETPKVTEKAYFPIVETIUKERIPFGNITGTYLTKLPKID 60
Db 1 LRALYFHNQYAEIPKSEPKVIEKAYFPIVETIUKERIPFGNITGTYLTKLPKID 60

Qy 61 LVGGGIASDIEIIGTSYTHAILPLPLSPRVEAQVORDREVKELFPEVSPKGWLPETAY 120
Db 61 LVGGGIASDIEIIGTSYTHAILPLPLSPRVEAQVORDREVKELFPEVSPKGWLPETAY 120

Qy 121 DRIIPAIKONGYEVIFADPGRAMLSAHNSATKPIKPYPHLKAQERKRFRYISYLG 180
Db 121 DRIIPAIKONGYEVIFADPGRAMLSAHNSATKPIKPYPHLKAQERKRFRYISYLG 180

Qy 181 LRLRRAIKLVFEGKTLKAVDIEAPVWVANTAVMIGIGRPLMNPWQKVASIEDKD 240
Db 181 LRLRRAIKLVFEGKTLKAVDIEAPVWVANTAVMIGIGRPLMNPWQKVASIEDKD 240

Qy 241 NILLYGTDIEFIGYRDIAGRMSVEGLLEIDELNSCLPSEKLSKGELYKRTSSWAP 300
Db 241 NILLYGTDIEFIGYRDIAGRMSVEGLLEIDELNSCLPSEKLSKGELYKRTSSWAP 300

Qy 301 DKSLSRTRWEDSGNARLMLSTMGRGLAFLAENDSARGWPLPERRIDAFAIRAINDWRC 360
Db 301 DKSLSRTRWEDSGNARLMLSTMGRGLAFLAENDSARGWPLPERRIDAFAIRAINDWRC 360

Qy 361 NCEP 364
Db 361 NCEP 364

RESULT 12
US-10-282-122A-53281
; Sequence 53281, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848

RESULT 13
US-10-369-493-23237
; Sequence 23237, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10 (52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374

PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SEQ ID NO: 53281
; LENGTH: 890
; TYPE: PRT
; ORGANISM: Clostridium difficile
; US-10-282-122A-53281

Query Match 5.9%; Score 111.5; DB 15; Length 890;
Best Local Similarity 23.6%; Pred. No. 0.57; Mismatches 72; Conservative 48; Indels 87; Gaps 16; Matches 72;

Qy 53 FUPKIDILVKGGIASDIEIIGTSYTHAILPLPLSPRVEAQVORDREVKELFPEVSPKG 112
Db 562 FOP-DLTIAVGGCSAMDAKGKINWVWHEPEVDQDLA-----MRFMDIRKRVY-VFPK- 612

Qy 113 FWLPELAYDPIP-----KLL-KDNGYEVLEPAGEAMMFSAHNSATKPIK 158
Db 613 -NGEKAYFAAFLPITSAGTGSEYTPFAVITDODSGVKYPLADYELPMNMAIIDADMNEMP 670

Qy 159 LYPLH-----IKQREKRFRYISYLG-----LGRERLRAIKLVF-----GKVTL 198
Db 671 -PRITAASGVDALTHALEAVYSLMRTEPADGLA---QAGKIIPEYLPRAYKGKNDK 724

Qy 199 KAYVEDIAEVWVANTA-----VMLIGRLPMM-----P 229
Db 725 EAREKMMAMASTMAGMSTFANAFLGICHLAKUGFHIVQHGIVANALLINEVKFNCLEAP 784

Qy 230 KRYASWIEDK-----PNTLIGTDIEFIGYRDIAGY--RMSVEGLIEVIDEELNSCLPSEKL 285
Db 785 NROMGAPSQYRYPDCIORYA--EFASAGIKGSTDQVKUNIKAIDSLKARVQFPTIK 841

Qy 286 HSGRE 290
Db 842 EAGVE 846

;

; SEQ ID NO 23237

; LENGTH: 312

; TYPE: PRT

; ORGANISM: *Bacillus subtilis*

US-10-369-493-23237

Query Match 5.8%; Score 109; DB 14; Length 312;
Best Local Similarity 23.2%; Pred. No. 0.22; Mismatches 58; Indels 56; Gaps 9;
Matches 44; Conservative 32; Mismatches 58; Indels 56; Gaps 9;

Qy 10 LQYAEIPKSEIPK-----VIEKAYIPIVIELIKEEIPFGNLNTGYTLKFLPKDIDI 61
Db 130 MTYAVYKESGFPKERIVGQSGVLDTR--PRTIVAAE---LNIS-----VKDVTF 175

Qy 62 VKGGIASDLSLIELIGTSYTHA---LPLPLSVAEQVQDRREVKEELFEVSPKG--FWLPS 117
Db 176 VLGHHGDDMVLVRYSYAGGIPLETIPIKERIDAIVTRTKGGETVNLLNGSAYAPA 235

Qy 118 LAYDPITPAIILKDN-----GIEYLF-----ADGFAMLSS-----A 147
Db 236 ASLTVENEAELKDQRRVLIPIAYLEGEYVGIGIVLGVPTIVGGNGLEQITELTDYERA 295

Qy 148 HLNSATKPKI 157
Db 296 QLNKSVESVK 305

RESULT 14
US-10-425-115-291380
; Sequence 291380, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 291380
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(590)
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: MRT457_28825C.1.pep
US-10-425-115-291380

Query Match 5.6%; Score 105.5; DB 15; Length 573;
Best Local Similarity 21.3%; Pred. No. 1.1; Mismatches 97; Indels 131; Gaps 19;
Matches 77; Conservative 57; Mismatches 97; Indels 131; Gaps 19;

Qy 6 FHNGL-QYAEIPKS---EIPKVIKAYIPIV-----IETL 35
Db 290 FLSGKGLGKVPSGLSGLSVPPISPYWCPPRISTCSIAATQSPRSSIET 349

Qy 36 IKEPKIPGLNTGYTLKFLPKDIDIYLUKGSGIASDLSLIELIGTSYTHA---LPLPS 95
Db 350 ---PPFSGASILANPLS-----VNL-----DPVQPLGTSMDPP--DFLP-----DPLV 388

Qy 96 QDRDVEEELRVEVKGFWRELAYDI--IPAI-LKDNEYEVIFADGEAMLFKHLNSA 152
Db 389 RMSLUTPSQOLPTPFB-----LMDPDIYHVPVDPVCSSGQGYVAGPAMSPS----- 435

Qy 153 IKPKIPLYPLIKAQERKRFRYVSYLVLGRELKAIKLVFEG-----KVTLKAVKD 203
Db 436 --IPFLHPLVKEPLIPESDAW-----KGARETRILILSSQSQNQMRDTPAI-- 484

Qy 204 IAEAVWVWVANTAVNLGIGRLPLAMPKVVASWIDKDNTILYGDIEFTGYRD----- 257
Db 485 -----LNPD-----LNPD-----BQNNTIVAGSRRGLYNGTRDNTIANS 516

Qy 258 --AGYRMVSGGLELDEINSELCPSEKHSGBELRBTSSWAPSKSLRIRWDEGNR 315
Db 517 TAAMGIVLVSLSGVSKVSGVYSEL---ENYGNLEAVKSN--DSCGGAFLDDEGSS 568

Qy 316 LN 317
Db 569 LD 570

Query Match 5.6%; Score 106; DB 17; Length 590;
Best Local Similarity 23.3%; Pred. No. 1; Mismatches 59; Conservative 46; Indels 54; Gaps 13;
Matches 59; Conservative 46; Mismatches 59; Indels 54; Gaps 13;

Qy 22 KVIKEKAYIPIVIELIKEIPLKDI-----EEIPGLNTGYTLKFLPKDIDIYLUKGSGIASDLSLIELIGT 76
Db 343 KKAQGGYTHLVAIDKFTKWEYKPLASLTSKAKAEPF-I-QDII--FRFGFPNSITDIGS 399

Qy 77 SYTHATL-----PLPLSLRVEAQVOR-----PREVKELFEPSPK--GPMLP 116
Db 400 NFTSBEFFDFCEQRSTQIKVAKSLAHPRANGCOVERANGMIREALRKKVFDKNEKFVKGWIR 459

Qy 117 BLAYDPIIPAIKLDQNGYBLF--ADGEA-----MLFSAHNSAIKPTKPLVPHLKA 166
Db 460 ELPYVWVLPADLRFQAPRPLFESTAEEARLVEYDYLEERLNTVQSR--YQQTARR 517

Qy 167 OREKRFRYVSYLGLGRELKAIKLVFEGKVTLKAVKVDIEAVPVW--VAVNTAVMLGIGR 223
Db 518 YHDKTRHRSPFVNGDVLVRRI--LTCGEGRKLS-----PQWEGPPFMVSEVTRPGSIR 567

RESULT 15
US-10-424-599-175517
; Sequence 175517, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 175517
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12950C.1.pep
US-10-424-599-175517

Query Match 5.6%; Score 105.5; DB 15; Length 573;
Best Local Similarity 21.3%; Pred. No. 1.1; Mismatches 97; Indels 131; Gaps 19;
Matches 77; Conservative 57; Mismatches 97; Indels 131; Gaps 19;

Qy 6 FHNGL-QYAEIPKS---EIPKVIKAYIPIV-----IETL 35
Db 290 FLSGKGLGKVPSGLSGLSVPPISPYWCPPRISTCSIAATQSPRSSIET 349

Qy 36 IKEPKIPGLNTGYTLKFLPKDIDIYLUKGSGIASDLSLIELIGTSYTHA---LPLPS 95
Db 350 ---PPFSGASILANPLS-----VNL-----DPVQPLGTSMDPP--DFLP-----DPLV 388

Qy 96 QDRDVEEELRVEVKGFWRELAYDI--IPAI-LKDNEYEVIFADGEAMLFKHLNSA 152
Db 389 RMSLUTPSQOLPTPFB-----LMDPDIYHVPVDPVCSSGQGYVAGPAMSPS----- 435

Qy 153 IKPKIPLYPLIKAQERKRFRYVSYLVLGRELKAIKLVFEG-----KVTLKAVKD 203
Db 436 --IPFLHPLVKEPLIPESDAW-----KGARETRILILSSQSQNQMRDTPAI-- 484

Qy 204 IAEAVWVWVANTAVNLGIGRLPLAMPKVVASWIDKDNTILYGDIEFTGYRD----- 257
Db 485 -----LNPD-----LNPD-----BQNNTIVAGSRRGLYNGTRDNTIANS 516

Qy 258 --AGYRMVSGGLELDEINSELCPSEKHSGBELRBTSSWAPSKSLRIRWDEGNR 315
Db 517 TAAMGIVLVSLSGVSKVSGVYSEL---ENYGNLEAVKSN--DSCGGAFLDDEGSS 568

Search completed: January 27, 2005, 05:59:41
Job time : 65 secs

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OM protein - protein search, using SW model
Run on: January 27, 2005, 05:58:26 ; Search time 22 seconds
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RESULT 2
 US-10-112-231A-4
 ; Sequence 4, Application US/10112231A
 ; Patient No. 674246
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Dennis
 ; APPLICANT: Reid, John
 ; TITLE OF INVENTION: ALPHA GALACTOSIDASES AND METHODS FOR
 ; FILE REFERENCE: 0901-004005
 ; CURRENT APPLICATION NUMBER: US/10/112,231A
 ; CURRENT FILING DATE: 2002-03-29
 ; PRIORITY NUMBER: US 09/407,806
 ; PRIORITY FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 4
 ; SEQ ID NO 4
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Thermococcus alcaliphilus
 ; US-10-112-231A-4

Query Match 100.0%; Score 1879; DB 4; Length 364;
 Best Local Similarity 100.0%; Pred. No. 4_9e-191; Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRALVFGNQYAEIPKSEIPKVKIRAYPVVIETLKEETPFGNINITYGTYLKFLPKDID 60
 Db 1 LRALVFGNQYAEIPKSEIPKVKIRAYPVVIETLKEETPFGNINITYGTYLKFLPKDID 60
 Qy 61 LVGGTASDIEIIGSYTHTAILPLPLSRVEAQVDRVEKFLFEVSPKGFWLPELAY 120
 Db 61 LVGGTASDIEIIGSYTHTAILPLPLSRVEAQVDRVEKFLFEVSPKGFWLPELAY 120
 Qy 121 DPITPAIKONGYEVLFADGEAMLSAHNSAIKPKPLYPHLTKAQERKFRYISVLG 180
 Db 121 DPITPAIKONGYEVLFADGEAMLSAHNSAIKPKPLYPHLTKAQERKFRYISVLG 180
 Qy 181 LRELRKAIKUVFEGKVTLKVKDIEAVPVWAVVNTAVMLGIGRPLMNPKVASIEDKD 240
 Db 181 LRELRKAIKUVFEGKVTLKVKDIEAVPVWAVVNTAVMLGIGRPLMNPKVASIEDKD 240
 Qy 241 NILYGTDFIPIGRDIAIGRMSVGEGLLEVVIDELSELCPSELKHSRELYRTSSWAP 300
 Db 241 NILYGTDFIPIGRDIAIGRMSVGEGLLEVVIDELSELCPSELKHSRELYRTSSWAP 300
 Qy 301 DKSRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPURRLDAFRAYNDWGE 360
 Db 301 DKSRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPURRLDAFRAYNDWGE 360
 Qy 361 NGEP 364
 Db 361 NGEP 364

RESULT 3
 US-08-613-220B-4
 ; Sequence 4, Application US/08613220B
 ; Patient No. 5958751
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Dennis
 ; APPLICANT: Reid, John
 ; TITLE OF INVENTION: ALPHA-GALACTOSIDASE
 ; NUMBER OF SEQUENCES: 4

Query Match 84.6%; Score 1589; DB 2; Length 346;
 Best Local Similarity 95.1%; Pred. No. 3.1e-160; Matches 346; Conservative 0; Mismatches 0; Indels 18; Gaps 18;

Qy 1 LRALVFGNQYAEIPKSEIPKVKIRAYPVVIETLKEETPFGNINITYGTYLKFLPKDID 60
 Db 1 LRALVFGNQYAEIPKSEIPKVKIRAYPVVIETLKEETPFGNINITYGTYLKFLPKDID 60
 Qy 61 LVGGTASDIEIIGSYTHTAILPLPLSRVEAQVDRVEKFLFEVSPKGFWLPELAY 120
 Db 61 LVGGTASDIEIIGSYTHTAILPLPLSRVEAQVDRVEKFLFEVSPKGFWLPELAY 120
 Qy 121 DPITPAIKONGYEVLFADGEAMLSAHNSAIKPKPLYPHLTKAQERKFRYISVLG 180
 Db 121 DPITPAIKONGYEVLFADGEAMLSAHNSAIKPKPLYPHLTKAQERKFRYISVLG 180
 Qy 181 LRELRKAIKUVFEGKVTLKVKDIEAVPVWAVVNTAVMLGIGRPLMNPKVASIEDKD 240
 Db 181 LRELRKAIKUVFEGKVTLKVKDIEAVPVWAVVNTAVMLGIGRPLMNPKVASIEDKD 240
 Qy 241 NILYGTDFIPIGRDIAIGRMSVGEGLLEVVIDELSELCPSELKHSRELYRTSSWAP 300
 Db 241 NILYGTDFIPIGRDIAIGRMSVGEGLLEVVIDELSELCPSELKHSRELYRTSSWAP 300
 Qy 301 DKSRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPURRLDAFRAYNDWGE 360
 Db 301 DKSRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPURRLDAFRAYNDWGE 360
 Qy 361 NGEP 364
 Db 361 NGEP 346

RESULT 4
 US-07-894-212A-8
 ; Sequence 8, Application US/07094212A
 ; Patent No. 5366883

GENERAL INFORMATION:

APPLICANT: ASADA, KIYOSO
 APPLICANT: UEMORI, TAKASHI
 APPLICANT: MUKAI, HIROYUKI
 APPLICANT: KATO, IKUNOSHIN
 APPLICANT: LADERMAN, KENNETH
 APPLICANT: ANFINSEN, CHRISTIAN
 TITLE OF INVENTION: THE ALPHA-AMYLASE GENE
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON, D.C.
 COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/894, 212A
 FILING DATE:
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REFERENCE/DOCKET NUMBER: 16773
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 647 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-894-212A-8

Query Match

Best Local Similarity 7.5%; Score 140.5; DB 1; Length 647;
 Matches 89; Conservative 60; Mismatches 127; Indels 115; Gaps 23;

Qy 25 EKAYPIVIETLKEISP--FGLNITGYTKFLP--KOIDILVKCGIASSDLIERIGTSY 78
 Db 27 EKCYWPFLETL--EYPVNMKVAHTSGPYLEWLDNRPVYDILRSVKGQEVIVAGF 84

Qy 79 THAIIPLPLPSRVEAQVQDRREVKE--ELFVSPKGFWLPLBLAYDPIPAIKLKGYEV 136
 Db 85 YEPVLASIP--KEDRIEQIRLMKEWAKSIGFARGWMLTERVWQPELVKTLKESGIDV 141

Qy 137 FADGHEMLFAHNSAIKPKPLY-PHLIKAQE-----KFRYIYSTLGLRLERLKA 187
 Db 142 IVD----DYHFMSSAGLSKELIWPYTYTEDGEDEVIAVPIDEKLR--YLIPRPVDKV 192

Qy 188 IKL--VFECKVTKAV--KDIENAIVPVWVAVNTAVMLGIGRLPLMNPKKVASW 236
 Db 193 LEYLIHSLIDDESKVAFVHDFGEKGIGIWPOTYEWY-----EKGMLREFEDR 239

Qy 237 ---EDKDNLILYGYDIE----FIGYRDAGYRMSVEGLIEVIDELNSELICLP----- 281
 Db 240 ISSDEKINLMLYTYELEKVKPRLVYLPIASY-----FEM----SEWSLPAKQARLF 287

Qy 282 ---SELKHSG---RELYKRTSSWAPDKSLR1WREDEGN--ARLNMSLYNNMGEFLAFL 330
 Db 288 VEFVNELKVKGIFEKYRVRVFRGGIW---KMF-FYKYPESNMHMKRMVMSKLVNN--- 339

Qy 331 AENSARGWMLPPLPERLDARAIYND--WKG 359
 Db 340 -----PEARKYLLRAQCDUAYWIG 358

RESULT 5

US-07-894-212A-2

Sequence 2, Application US/07894212A

Patent No. 536683

GENERAL INFORMATION:

APPLICANT: ASADA, KIYOSO

APPLICANT: UEMORI, TAKASHI

APPLICANT: MUKAI, HIROYUKI

APPLICANT: KATO, IKUNOSHIN

APPLICANT: LADERMAN, KENNETH

APPLICANT: ANFINSEN, CHRISTIAN
 TITLE OF INVENTION: THE ALPHA-AMYLASE GENE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN

CITY: WASHINGTON, D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/894, 212A
 FILING DATE:
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REFERENCE/DOCKET NUMBER: 16773
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 649 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-894-212A-2

Query Match 7.5%; Score 140.5; DB 1; Length 649;
 Matches 89; Conservative 60; Mismatches 127; Indels 115; Gaps 23;

Qy 25 EKAYPIVIETLKEISP--FGLNITGYTKFLP--KOIDILVKCGIASSDLIERIGTSY 78
 Db 29 EKCYWPFLETL--EYPVNMKVAHTSGPYLEWLDNRPVYDILRSVKGQEVIVAGF 86

Qy 79 THAIIPLPLPSRVEAQVQDRREVKE--ELFVSPKGFWLPLBLAYDPIPAIKLKGYEV 136
 Db 87 YEPVLASIP--KEDRIEQIRLMKEWAKSIGFARGWMLTERVWQPELVKTLKESGIDV 143

Qy 137 FADGHEMLFAHNSAIKPKPLY-PHLIKAQE-----KFRYIYSTLGLRLERLKA 187
 Db 144 IVD----DYHFMSSAGLSKELIWPYTYTEDGEDEVIAVPIDEKLR--YLIPRPVDKV 194

Qy 188 IKL--VFECKVTKAV--KDIENAIVPVWVAVNTAVMLGIGRLPLMNPKKVASW 236
 Db 195 LEYLIHSLIDDESKVAFVHDFGEKGIGIWPOTYEWY-----EKGMLREFEDR 241

Qy 237 ---EDKDNLILYGYDIE----FIGYRDAGYRMSVEGLIEVIDELNSELICLP----- 281
 Db 242 ISSDEKINLMLYTYELEKVKPRLVYLPIASY-----FEM----SEWSLPAKQARLF 289

Qy 282 ---SELKHSG---RELYKRTSSWAPDKSLR1WREDEGN--ARLNMSLYNNMGEFLAFL 330
 Db 290 VEFVNELKVKGIFEKYRVRVFRGGIW---KMF-FYKYPESNMHMKRMVMSKLVNN--- 341

QY 331 AENDSARGWEPPLRRRDAFRAILYND--WRG 359
 Db 342 -----PEARKYLRAQCNDAYWHD 360

RESULT 6
 US-07-893-928A-1
 ; Sequence 1, Application US/07893928A
 ; Patent No. 5378479
 ; GENERAL INFORMATION:
 ; APPLICANT: LADERMAN, KENNETH
 ; TITLE OF INVENTION: a-AMYLASE FROM HYPERTHERMOPHILIC
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON, D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Tape
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/893, 928A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KORULIS, PAUL N.
 ; REGISTRATION NUMBER: 16773
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 861-3000
 ; TELEFAX: (202) 822-0344
 ; TELEX: 6714627 CUSH
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 650 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-893-928A-1

Query Match 7.5%; Score 140.5; DB 1; length 650;
 Best Local Similarity 22.8%; Pred. No. 8.7e-05;
 Matches 89; Conservative 60; Mismatches 127; Indels 115; Gaps 23;

QY 25 EKAYIPVTFIILIKEKIP---FGLNITGYLKFELP---KDIIDIVKGGLASDLEIIGTSY 78
 Db 29 EKCIWPPFEL---EYPNMKVAKHNSGPLEWLQDNRPHEYIDLRSILVKRGGEYIWAGF 86
 QY 79 THAIPLPLPSRVAQVQREREVKE---ELFEVSPKGFLPFLPFLAYDPPIPATLKDNGEYEL 136
 Db 87 YEPVLASIP---KEDRIEQRLMKWAKASIGDARGWMLTWRQPELPUVKTKESGIDYV 143

QY 137 FADGBAMFSAHNSAIKPKIYKPHIKAQRE-----KFRFTSYLIGLRLRKA 187
 Db 144 IVD-----DHYENSAQGLSKELLYWPPYTDGSEVIAVFPIDBK---YLIIPFRPVK 194
 QY 188 IKL---VIEGGKVTKAV---KDIAVPUVVAVNTAVMGLGIGRPLMNPKKVASYI----- 236
 Db 195 LEVHSLIDGDSKAVVFRDGEKFGKIGWPGTIEWVY-----EKGWLREFPDR 241

QY 237 ---EDKDNILYLYGTDIE---FIGYRDIAGIYRMSVEGLIYEVITDELNSLCLP----- 281
 Db 242 ISSDEKINILMLYTYELEKVKPGLVLYPIASY-----FEM-----SEWLPQKQARLF 289

QY 282 ---SELKHSG---REVIKRTSSWAPDKSURIWREDEGN---ARJNMLSNMRGELAFL 330

Db 290 VEFVNLKVKGIFERKXYRUFVRGGTw---KNF-FYKYPEBNYMHKRMJLNVSKLVRRN--- 341
 QY 331 AENDSARGWEPPLRRRDAFRAILYND--WRG 359
 Db 342 -----PEARKYLRAQCNDAYWHD 360

RESULT 7
 US-09-107-532A-5554
 ; Sequence 5554, Application US/09107532A
 ; Patent No. 6583775
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; NUMBER OF SEQUENCES: 7310
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02454
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD/DOM ISO9660
 ; COMPUTER: PC
 ; OPERATING SYSTEM: <Unknown>
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/107, 532A
 ; FILING DATE: 30-Jun-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/085, 598
 ; FILING DATE: 14 May 1998
 ; APPLICATION NUMBER: 60/051571
 ; FILING DATE: July 2, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ainiello, Pamela Denreke
 ; REGISTRATION NUMBER: 40, 489
 ; REFERENCE/DOCKET NUMBER: GTC-012
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781)893-5007
 ; TELEFAX: (781)893-8277
 ; INFORMATION FOR SEQ ID NO: 5554:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 227 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: Enterococcus faecium
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (B) LOCATION 1...227
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5554:
 ; US-09-107-532A-5554

Query Match 5.6%; Score 105; DB 4; length 227;
 Best Local Similarity 24.2%; Pred. No. 0.0095;
 Matches 60; Conservative 34; Mismatches 88; Indels 66; Gaps 12;

QY 140 GEAMFLSAHNSAIKPKIYKPHIKAQREKRFTSYLIGLRLRKA-----AI 188
 Db 3 GEKMFSTITWKL-----GGLIGLIVLVRIGKMSSELTPDLYV 43

QY 189 KLVFGKVTKAVKD-----TEAVPWWAVNTAVMGLGIGRPLMNPKKVASYIWDKD 240
 Db 44 TLVIGGLIBESTYDYNVHGVHLIAJW---AVMVGIERIVQK-EKVRWVKGEP 97

QY 241 NILYGTIDFIGYRDIAGIYRMSVEGLIYEVITDELNSLCLP-----LKTSGREYLT 294

Db 98 SVLIKD---GVINMELINNIEMEOLRAI---LROQBCIPLENKHLVILENAGOMSVLK 151
 Qy 295 TSSWAPDKSRIWREDEGNARLNMSYMMRGEFLAENDARGHEPLPERRDLFRAIY 354
 Db 152 KSD---EDKALISLLVDEGQIQLHKVLOSNOLTE-ANWLMNLKKEY-----ADYKOLY 201
 Qy 355 NDWRGNG 362
 Db 202 VEWSEBKG 209

RESULT 8
 US-09-710-279-2150
 ; Sequence 2150, Application US/09710279
 ; Patent No. 6703492
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMELLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEAR ACIDS AND PROTEINS
 ; FILE REFERENCE: FU3490US
 ; CURRENT APPLICATION NUMBER: US/09/710,279
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2150
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 ; US-09-710-279-2150

Query Match 5.4%; Score 101.5; DB 4; Length 376;
 Best Local Similarity 19.1%; Pred. No. 0.05; Mismatches 117; Indels 73; Gaps 12;
 Matches 57; Conservative 52; Mismatches 117; Indels 73; Gaps 12;

Query Match 5.4%; Score 101.5; DB 4; Length 376;
 Best Local Similarity 19.1%; Pred. No. 0.05; Mismatches 117; Indels 73; Gaps 12;
 Matches 57; Conservative 52; Mismatches 117; Indels 73; Gaps 12;

Matches 57; Conservative 52; Mismatches 117; Indels 73; Gaps 12;
 Query 4 LVERGNLQYKBIKSEIPIKVKIEKAVIPIVETLKEIPPGNITGTYTLKFLPKDIDLYK 63
 Db 61 LIFKG-----VKRIVEDGYSIRKLQIINN--NLIALHTNLDVNPKGVNRMIA 93
 Qy 64 GGIADDIEIIGT-SYTHAILPLPLRSVAQVDRKEELREVSKPGPMRELAYD 121
 Db 94 DQIGHENISNINTSSYYVQTFIPKPYIE-----DFPKDSNEL----- 133
 Qy 122 PIPIAIIKONGYEVIFADGEAMLSFSAHNSAIKPIKPLVPHLIKQREKFRYISYLL3L 181
 Db 134 ---GLAKEGENYKCFPESBG-----KGQPKPVGDAPIGLDS-----IEVY--- 173
 Qy 182 RELRIKAIKUW-----EGKOTLKAVKDIE-AVYV--WVAINTAVMLGIGRLPLMPKKV 232
 Db 174 ---DEIKLEFMKONNELEITKRAILNDHNPYETPVDFIKNNKESBYGLGIGQNTMT 229
 Qy 233 ASWIKEDKNDLILYDIEFGYRIRAGMSVEGLIEV---IDELENSELCLSELKH 286
 Db 230 LDEFSEYYAKQKLNIPSPVRYQHDSPIKKVAILGGSGIGREYKASQLGADVFTGDIK 288

RESULT 9
 US-09-270-013B-2
 ; Sequence 2, Application US/08270013B
 ; Patent No. 5686294
 ; GENERAL INFORMATION:
 ; APPLICANT: Sogabe et al.
 ; TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
 ; STREET: Two Prudential Plaza, Suite 4900
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 61601-6780
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/270,013B
 ; FILING DATE: 01-JUL-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 164701/1993
 ; FILING DATE: 02-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Green, Robert F.
 ; REGISTRATION NUMBER: 27555
 ; REFERENCE/DOCKET NUMBER: 62321
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 616-5700
 ; TELEFAX: (312) 616-5700
 ; TELEX: (25) 3533
 ; INFORMATION FOR SEQ ID NO: 2:
 ; LENGTH: 329 amino acids

RESULT 9
 US 09-710-279-2106
 ; Sequence 2106, Application US/09710279
 ; Patent No. 6703492
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMELLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEAR ACIDS AND PROTEINS
 ; FILE REFERENCE: FU3490US
 ; CURRENT APPLICATION NUMBER: US/09/710,279
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-270-013B-2

Query Match 5.4%: Score 101; DB 1; length 329;
 Best Local Similarity 25.3%; Pred. No. 0.046; Length 329;
 Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

QY 10 LQYAEPKSEIPK-----VIEKAYIPVIETLIKEBIPFGLNITGTYTLKFLPKDIDL 61
 Db 130 MTYVTFKSGFPKRNVRIGQSGVLDTAR--FRTFVABE---LNIS-----VKDTWGP 175
 Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

QY 62 VKGGIASDLIELIGTSYTHAI--LPLPLPLSRVAVQVDRDVEKELFPEVSPKG--FVLPF 117
 Db 176 VLGGHGDMDMPLVRYSYAGGIPLEKLIKPKDRLDAIVTRKGGEIVNLNGNSAYAPA 235
 Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

QY 118 LAYDPTIPAILKDN-----GYELF 137
 Db 236 ASLVEVNEAILKQORRILPAIAYLEGEYGYEGIY 269
 Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

RESULT 11
 US-08-838-418-2

Sequence 2, Application US/08838418
 Patent No. 5744342

GENERAL INFORMATION:

APPLICANT: Segabe et al.
 TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE DEHYDROGENASE ACTIVITY

APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA.

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60601-6780

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,418
 FILING DATE: 17-MAR-1997
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 164701/1993
 FILING DATE: 02-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoover, Allen E.
 REFERENCE/DOCKET NUMBER: 37354
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 616-5600
 TELEX: (25) 3533

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 329 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-418-2

Query Match 5.4%: Score 101; DB 1; length 329;
 Best Local Similarity 25.3%; Pred. No. 0.046; Length 329;
 Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

QY 10 LQYAEPKSEIPK-----VIEKAYIPVIETLIKEBIPFGLNITGTYTLKFLPKDIDL 61
 Db 130 MTYVTFKSGFPKRNVRIGQSGVLDTAR--FRTFVABE---LNIS-----VKDTWGP 175
 Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

QY 62 VKGGIASDLIELIGTSYTHAI--LPLPLPLSRVAVQVDRDVEKELFPEVSPKG--FVLPF 117
 Db 176 VLGGHGDMDMPLVRYSYAGGIPLEKLIKPKDRLDAIVTRKGGEIVNLNGNSAYAPA 235
 Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

QY 118 LAYDPTIPAILKDN-----GYELF 137
 Db 236 ASLVEVNEAILKQORRILPAIAYLEGEYGYEGIY 269
 Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

RESULT 12
 US-09-540-236-3128

Sequence 3128, Application US/09540236
 Patent No. 667910

GENERAL INFORMATION:
 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA.

CURRENT APPLICATION NUMBER: US/09/540,236

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 3128

LENGTH: 653

TYPE: PRT

ORGANISM: M. catarrhalis

US-09-540-236-3128

Query Match 5.2%: Score 97; DB 4; Length 653;
 Best Local Similarity 21.9%; Pred. No. 0.37; Length 653;
 Matches 72; Conservative 43; Mismatches 128; Indels 86; Gaps 13;

QY 22 KTEKAYIPVIETLIKEBIPFGLNITGTYTLKFLP-----KDIIDLVGGTAS--- 68
 Db 95 KRIEPAVRGIVTD--REGAAPLAANAPLYTFDPAYAEYVYRLDNEIKTKSEPAKQKA 152
 Matches 72; Conservative 43; Mismatches 128; Indels 86; Gaps 13;

QY 69 -----DLIEITGTSYTHAI--LPLPLPLSRVAVQVDRD-----REVKELFPEVSPKG 113
 Db 153 LKKLKDENDLVL-----AAVANTPLEKLEAVGIDHTDTSNSQVKRAL---PKGA 201
 Matches 72; Conservative 43; Mismatches 128; Indels 86; Gaps 13;

QY 114 WLPFLA-YDPTIPAILKDNGYEYLADGEAMLSAHLNSAIKPKLYPHIKAOREKRP 172
 Db 202 SSRLVLVLRNRSPEVAKSVTDLGLFAIGRBSQYFORYLQ-EPNAQOLGYSWADSDTQG 260
 Matches 72; Conservative 43; Mismatches 128; Indels 86; Gaps 13;

QY 173 RYISVYLGRLRKLAKLKVVEGKVTLKAVKDIIEAVPVWVANTAVMLGIGRLPLMNPKV 232
 Db 261 GYIG-----RAGIEAKNERNLAGKDGK-----VOLRSGRQPOEQI 300
 Matches 72; Conservative 43; Mismatches 128; Indels 86; Gaps 13;

QY 233 ASWIEDKDNILLYLGTDIEFYGRDIAQYRMSVEGLLEDELNLSBLCPSELKHSGRELY 292
 Db 301 EPLICENRITRIDERLYQVLYKE-----LBQVGRLO-----SARSSGMVVD 343
 Matches 72; Conservative 43; Mismatches 128; Indels 86; Gaps 13;

QY 293 LRT-----SSWADPKSLRIRWREDEGNAR 315
 Db 344 VKTGEVILAMGSWPSFNSNNLSELDRGANE 372
 Matches 72; Conservative 43; Mismatches 128; Indels 86; Gaps 13;

RESULT 13
 US-09-134-001C-3678

Sequence 3678, Application US/09134001C
 Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Staam et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

FILE REFERENCE: GTC-C-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 3678
; LENGTH: 367
; TYPE: PRT
; ORGANISM: *Staphylococcus epidermidis*
; US-09-134-001C-3678

Query Match Similarity 5.0%; Score 94.5; DB 3; Length 367;
Best Local Similarity 18.7%; Pred. No. 0.27; Mismatches 118; Indels 73; Gaps 12;
Matches 56; Conservative 52; MisMatches 118; Indels 73; Gaps 12;

Qy 4 LVPHGMLQYAIKPSEIPKVEKAYIPVIETIKEIPIFGUNITGTYLKLKPDKIDLUK 63
Db 68 LIFKG-----VKRIVEDGYGSIRKLIQNNI-NIHALHNTDYNPKGVNRMILA 114

Qy 64 CGIASDLIEIIGT-SYTHATIPLPLSRVQAQDREVKEELFPEVSPKGFWLPBELAYD 121
Db 115 DQIGENIISMINTNSSYVYQTFIPKNI-----DPIQDSNL----- 154

Qy 122 PIPIATKIDQYCEYLADGEAMLFSAHNSAIKPIKPLYPLIKOQREKFRYTSYLLG 181
Db 155 ---GLAKENSYEYCPFESEG-----KGOPGPVQDASPIYGKUDS-----IEVK----- 194

Qy 182 RELRKAIVP-----EGKVTIKAVIDE-AVPU-----WVAVNTAVMLGIGRLPMLPKV 232
Db 195 ---DEBKLFMVKONELTTRKAILDNPVTPYDFRINKKESBYGIGLIGIOLNQMT 250

Qy 233 ASWIEDKDNILLYGTDIEFIGRDIAGYRMSVEGLIEV-----IDELNSCLPSELKH 286
Db 251 LDEPSFYAKQKLNIPSVRYIQHDSPIKKVAKIIGGSGIGFYEKASQLGADPWFVGDIKH 309

RESULT 14

US-09-710-279-1840
; Sequence 1840; Application US/09710279
; Patent No. 6703492;
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERmidis NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS490US
; CURRENT APPLICATION NUMBER: US/09/710,279
; PRIORITY FILING DATE: 1999-11-09
; PRIORITY FILING NUMBER: US/09/248-796A-15394
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-09-710-279-1840

Query Match Similarity 4.9%; Score 92; DB 4; Length 845;
Best Local Similarity 20.2%; Pred. No. 1.9; Mismatches 117; Indels 128; Gaps 21;
Matches 78; Conservative 64; MisMatches 117; Indels 128; Gaps 21;

Qy 38 EELP-FGLNTGTYIUKFLPKDILVKGIASDLIEI-----GTSYTHAI 82
Db 202 DEMPHTGYDING-----KRMPIPKAGSADOLLESIBLPEGTGLPDONTGS----- 249

Qy 83 LPLPLSRVQAQDREVKEELF-VSPIKGFWLPBELAYDPIIAILKNDGKBYELFADGE 141
Db 250 ---LKLTDEELLELIRKIQQONTBNINP-----YEPLIDWFTK----- 286

Qy 142 AMLFLSAHNSAIKPIKPLYPLIKOQREKFRYTSYLLGRELKAIKLUPEGKV----- 196
Db 287 -----EEIMP-----VTAPEPKRPFVPSKHEAKRVMKVKAIREGRIPPNK 329

Qy 197 -----TKAVKTDIEAVPVW-----VAVNTAVM-LGIGRLP-----LMPKKVA 233
Db 330 VRQOLTTTBEEDOFNDMOWDEIBSDHIMNLRAPLKPPTNEESYNPPEEYUITEEKS 389

Qy 234 SWIB-----DKNILLYGTDIEFIGRDIAGYRMSVEGLIEVIDELNSCLPSELKHSGR 289
Db 390 KWLQSPSPDNERL-----PKQYNSLRQVGYQDSYRERF-----ERSLDYLAQPRVHN----- 440

Qy 290 ELYARTSSWAPD-----KSLR-----IWREDEGARNIAMLNSYMRGEBLAFLAENSP----- 335
Db 441 KUNIDPDSLDPDLSPPDKRPFPIRCSTYEGHTG-KIRTISIDPOG--LWLATGSDG 496

Qy 336 -ARGMPLEPLRRLAFAFLAYNDWGEN 361
Db 497 SVRIWEILTRQVYKQLINKEINNED 523

Qy 59 IDLVKGIGIADSLIELIGTSTYTHATIPLPLPSR-----EAQVQDREVKEELFEPSPK----- 111
Db 3 IDIESG-----DFIAFIGTSCSGKTTALRMNMRMESTEGEITIDGSKNIKLNPLVERSTI 58

Qy 112 GFWPLBLAYP-----IIPAIK-----DNGYELI----- 136
Db 59 GYVVIQIGLQPHMVTKENIVLVPKLUKWSQEKDEKAKEI-IRLVLPEELDRYPSLSC 118

Qy 137 -----FADGEAMLAFAHNSAIKPIKPHLTK--AQREKFRYTSYLLG 181
Db 119 GQQQIGVWVVALAABODIIMDEPGCALDITRDTIQLDLVKKLQQQLGKTFIFVTH----- 174

Sat Jan 29 08:32:13 2005

us-09-886-400a-4.rai

Search completed: January 27, 2005, 06:00:12
Job time : 28 secs

; ORGANISM: *Thermococcus alcaliphilus*
US-10-112-231A-3

Alignment Scores:

Pred. No.: 2.27e-209

Length: 1095

Matches: 364

Conservative: 0

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

Indels: 0

Gaps: 15

DB: US-09-886-400A-4 (1-364) x US-10-112-231A-3 (1-1095)

Qy 1 Leu Arg Gla Ile Val Phe His Gln Asn Leu Gln Tyr Val Ala Glu Leu Pro Leu Ser Gln Ile Ser

Db 901 Asp Lys Ser Leu Arg Ile Ile Phe Arg Glu Lys Asp Glu Val Ala Arg Leu Asn Met Leu Ser

Qy 321 TTT Asp Met Arg Gly Gln Ile Leu Ala Phe Leu Ala Glu Leu Asn Ser Asp Ala Arg Gly TTT Glu

Db 960 GAT AGAG CTG TTG GAG GAT ATG GAG AAG GCA GAG CCA GACT TAA TGT GTC

Qy 340 961 TAC KAT ATG GAG GGG GCA ACT CGC CT TTT TAC CG GAG AAG GCA GAG GAT CG GAG 1020

Db 341 Pro Leu Pro Glu Arg Arg Leu Asp Ala Phe Leu Ala Phe Leu Asn Asp Pro Arg Gly Gln 360

Qy 1021 CCC CT CCT CG AAG GAG GAG GCT GAT GCT TCC CG GCA TATA ACG TT GG GGT GAA 1080

Db 361 Asn Gly Glu Pro 364

Qy 1081 AAT CGG GAA CCT 1092

RESULT 2

US-09-886-400-3

; Sequence 3, Application US/09886400

; Patent No. US2002004526A1

; GENERAL INFORMATION:

; APPLICANT: DIVERSA CORPORATION

; APPLICANT: Murphy, Dennis

; APPLICANT: Ried, John

; TITLE OF INVENTION: ENYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE

; FILE REFERENCE: DIVER1120-4

; CURRENT APPLICATION NUMBER: US/09/886, 400

; CURRENT FILING DATE: 2001-06-20

; PRIORITY APPLICATION NUMBER: 09/619, 032

; PRIORITY FILING DATE: 2000-07-19

; PRIORITY APPLICATION NUMBER: 09/407, 806

; PRIORITY FILING DATE: 1999-09-20

; PRIORITY APPLICATION NUMBER: 08/613, 220

; PRIORITY FILING DATE: 1996-03-08

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO: 3

; LENGTH: 1095

; TYPE: DNA

; ORGANISM: *Thermococcus alcaliphilus*

; FEATURES:

; NAME/KEY: CDS

; LOCATION: (1) ... (1092)

US-09-886-400-3

Alignment Scores:

Pred. No.: 2.56e-208

Length: 1095

Matches: 362

Conservative: 1

Percent Similarity: 99.75%

Best Local Similarity: 99.45%

Query Match: 99.52%

DB: US-09-886-400A-4 (1-364) x US-09-886-400-3 (1-1095)

Qy 1 leu Arg Gla Ile Val Phe His Gln Asn Leu Gln Tyr Val Ala Glu Leu Pro Leu Ser Gln Ile Ser

Db 901 GAT AGAG CTG TTG GAG ATG GAG AAG GCA GAG CCA GACT TAA TGT GTC

Qy 321 TAC KAT ATG GAG GGG GCA ACT CGC CT TTT TAC CG GAG AAG GCA GAG GAT CG GAG 1020

Db 340 961 CCA AGG CTG TAG AGA GGG ATAC TCC CG TCA TGT GAG AAG GCA GAG GAT CG GAG 1080

Db 341 Pro Leu Pro Glu Arg Arg Leu Asp Ala Phe Leu Ala Phe Leu Asn Asp Pro Arg Gly Gln 360

Qy 1021 CCC CT CCT CG AAG GAG GAG GCT GAT GCT TCC CG GCA TATA ACG TT GG GGT GAA 1080

Db 361 Asn Gly Glu Pro 364

Qy 1081 AAT CGG GAA CCT 1092

; ORGANISM: *Thermococcus alcaliphilus*
US-10-112-231A-3

Alignment Scores:

Pred. No.: 2.27e-209

Length: 1095

Matches: 364

Conservative: 1

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: US-09-886-400A-4 (1-364) x US-10-112-231A-3 (1-1095)

Qy 1 leu Arg Gla Ile Val Phe His Gln Asn Leu Gln Tyr Val Ala Glu Leu Pro Leu Ser Gln Ile Ser

Db 901 GAT AGAG CTG TTG GAG ATG GAG AAG GCA GAG CCA GACT TAA TGT GTC

Qy 321 TAC KAT ATG GAG GGG GCA ACT CGC CT TTT TAC CG GAG AAG GCA GAG GAT CG GAG 1020

Db 340 961 CCA AGG CTG TAG AGA GGG ATAC TCC CG TCA TGT GAG AAG GCA GAG GAT CG GAG 1080

Db 341 Pro Leu Pro Glu Arg Arg Leu Asp Ala Phe Leu Ala Phe Leu Asn Asp Pro Arg Gly Gln 360

Qy 1021 CCC CT CCT CG AAG GAG GAG GCT GAT GCT TCC CG GCA TATA ACG TT GG GGT GAA 1080

Db 361 Asn Gly Glu Pro 364

Qy 1081 AAT CGG GAA CCT 1092

; ORGANISM: *Thermococcus alcaliphilus*
US-10-112-231A-3

PRIVILEGE: PROTECTED
 PRIORITY: 1
 PRIORITY FILING DATE: 2000-07-19
 PRIORITY APPLICATION NUMBER: 09/407, 806
 PRIORITY FILING DATE: 1999-09-20
 PRIORITY APPLICATION NUMBER: 08/613, 220
 PRIORITY FILING DATE: 1996-03-08
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3
 LENGTH: 1095
 TYPE: DNA
 ORGANISM: *Thermococcus alcaliphilus*
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: (1) .. (1092)
 US-10-112-357-3
 Alignment Scores:
 Pred. No.: 2.56e-208 Length: 1095
 Score: 1879.00 Matches: 362
 Percent Similarity: 99.73% Conservative: 1
 Best Local Similarity: 99.45% Mismatches: 1
 Query Match: 99.52% Indels: 0
 DB: 13 Gaps: 0
 US-09-886-4002-4 (1-364) x US-10-112-357-3 (1-1095)
 QY 1 Leu Arg Leu Val Phe His Glu Asn Leu Glu Tyr Ala Glu Leu Pro Leu Ser Glu Leu 20
 Db 1 TGAGAGC CCT CGT TT CAG SC AAC CTC AG AT CG CC GA AAC CCA AG GAG CCA ATC 60
 QY 21 Pro Leu Val Leu Glu Leu Ala Ser Leu Pro Val Leu Glu Thr Leu Leu Leu Glu Glu 40
 Db 61 CAAGGCA TAG AGG CCT AGT CCG AGT CTC AG CTC GAG ACT GAT GAG GCT AC 780
 QY 41 Pro Phe Glu Leu Asn Leu Thr Glu Tyr Thr Leu Leu Asp Leu Pro Leu Asp Leu Asp 60
 Db 121 CTT TGT GCT CTC AT CAG CTC GGT TAT ACT TAA GGT TCT CGG AGG AT TAT AG C 840
 QY 61 Leu Val Leu Val Phe His Glu Asn Leu Glu Tyr Ala Glu Leu Pro Leu Ser Glu Leu 80
 Db 181 CT CTT AA GGG GSC AT CG GAG GAC T GAG GAG GAT AT CG GAA CAC GAG TAC CG C 900
 QY 81 Ala Leu Pro Leu 100
 Db 61 CAAGGCA TAG AGG CCT AGT CCG AGT CTC AG CTC GAG ACT GAT GAG GCT AC 960
 QY 101 Val Leu Glu Leu Phe Leu Val Ser Asp Leu Pro Leu Leu Pro Leu Leu Pro Leu Leu 120
 Db 241 GCA TACT CCCC CCT CCG CT TAG CAG AG TAG A GAG A GAG C A G T C A G G A G T A G G A A T 1020
 QY 301 G T T A G G A G A G C T C C G A T T A G C C O G A C A G A C G T C A A S G A T C T G C G T C C G C T T 1040
 Db 301 G T T A G G A G A G C T C C G A T T A G C C O G A C A G A C G T C A A S G A T C T G C G T C C G C T T 1060
 QY 121 Asp Pro Leu Pro Leu Leu Leu Leu Asp 140
 Db 361 GACCGATAATCCCTGCCATCTGAGGAGCTGGCTCCGGCGATATATAAGATTTGGAGGGTGA 1080
 QY 141 Glu Lys Leu Phe Ser Lys Leu Lys Leu Lys Leu Lys Leu Lys Leu Lys Leu Lys 160
 Db 421 GAGGGGATGCTTCTCACTCTCACTCGGGATAAGCCATTAACCCCTAT 480
 QY 161 Pro Leu Leu Leu Asp 180
 Db 481 CACACTTAAAGGCCAAAGGAAAGGCCTTACGCTATGCTACGCTATCCTCTCT 540
 QY 181 Leu Arg Glu Leu Arg Glu Leu 200
 Db 601 GTCAAGAGATCGAGGCTTACCGTTGGCCGTCAGCGCTATAGCTCGCC 660
 QY 221 Ile Ile Arg Glu Leu Pro Leu Met Asn Pro Leu Val Leu Val Leu Val Leu Leu Leu 240
 Db 661 ATCGGAACTCTCTCTGAGCTTACGCTATGCTACGCTATCCTCTCT 720

RESULT 3
 US-10-112-357-3
 ; Sequence 3, Application US/10112357
 ; GENERAL INFORMATION:
 ; PUBLICATION NO. US20020115099A1
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: Murphy, Dennis
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH
 ; FILE REFERENCE: DIVER1120-4
 ; CURRENT APPLICATION NUMBER: US/10/112, 357
 ; PRIORITY FILING DATE: 2002-03-29
 ; PRIORITY APPLICATION NUMBER: 09/886, 400
 ; PRIORITY FILING DATE: 2001-06-20
 ; PRIORITY APPLICATION NUMBER: 09/619, 032

QY 241 AsnIleLeuLeuIleUryGlyThrAspIleGluPheIleGlyTyrAspAspIleAlaGlyTyr 260
 Db 721 AACATTCCTCTATAGGCACGGATATAGCTTCATGGCTATAGGACATGCAAGCTAC 780
 QY 261 ArgMetSerValGluGlyLeuIleLeuIleGluValIleAspIleGluAsnSerGluLeu 280
 Db 781 AGAATGAGTGTGAGGATTAAGGTATAGGCTATAGGAGGCTAACCGAACTGGCCT 840
 QY 281 ProSerGluLeuIleIshisArgIleGlyLeuIleLeuIleGluLeuAsnSerGluLeu 280
 Db 841 CCCCTAGAGCTGAACACAGCTGGAGGAGCTCTACTTGGACTCTGAGTGGCCTA 900
 QY 301 AspIleSerLeuIleIlePheAspGluIleAspGluIleAspIleLeuAsnMetLeuSer 320
 Db 901 GATAGAGCTTGAGCATAGAGGAGGAGGAGGACCCAGCTTAATATGGCT 960
 QY 321 TyrAsnMetArgGlyGluLeuIleLeuIleLeuIleGluLeuAsnSerGluLeu 340
 Db 961 TACATATAGGGGGCACTCGCCCTTTRAGCGGAGACGGGATGCAAGGGATGGGG 1020
 QY 341 ProLeuProGluArgArgLeuAspIlePheArgAlaIleTyrAsnAspIleArgGlyIle 360
 Db 1021 CCCCTCCCTGAGGAGGAGCTGGCTTCGGCGGATATAAGATGGAGGGTGA 1080
 QY 361 AspGlyGluPro 364
 Db 1081 ATGGGGAACT 1092

RESULT 4

US-10-114-403-3

Sequence 3: Application US/10114403
 Publication No. US20020115100A1
 GENERAL INFORMATION:
 APPLICANT: DIVERSA CORPORATION
 APPLICANT: Ried, John
 APPLICANT: Murphy, Dennis
 TITLE OF INVENTION: METHODS OF USE THEREOF
 FILE REFERENCE: DIVER1120-4
 CURRENT APPLICATION NUMBER: US/10/114, 403
 CURRENT FILING DATE: 2002-04-01
 PRIORITY APPLICATION NUMBER: 09/886,400
 PRIORITY FILING DATE: 2001-06-20
 PRIORITY APPLICATION NUMBER: 09/619, 032
 PRIORITY FILING DATE: 2000-07-19
 PRIORITY APPLICATION NUMBER: 09/407, 806
 PRIORITY FILING DATE: 1999-09-20
 PRIORITY APPLICATION NUMBER: 09/613, 220
 PRIORITY FILING DATE: 1998-03-08
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3 LENGTH: 1095
 TYPE: DNA
 ORGANISM: *Thermococcus alcaliphilus*
 FEATURE: NAME/KEY: CDS
 LOCATION: (1) . . . (1092)

US-10-114-403-3

Alignment Scores:
 Pred. No.: 2.56e-208 Length: 1095
 Score: 1870.00 Matches: 362
 Percent Similarity: 99.73% Conservative: 1
 Best Local Similarity: 99.45% Mismatches: 1
 Query Match: 99.52% Indels: 0
 DB: 13 Gaps: 0

US-09-886-400A-4 (1-364) x US-10-114-403-3 (1-1095)

QY 1 LeuArgAlaLeuValPheHisGlyAsnLeuIleUryAlaGluIleProIleSerGluLeu 20
 Db 21 ProLyValIleGluIleValIleUryIleProValIleGluIleLeuIleIleGluIle 40
 QY 61 CCAAGCTCATAGAGGCTACATCCAGCTCATCGAGAGCTTAAGTTCCTCCGGAGGAT 120
 Db 41 ProPhaglyIleAsnIleIleGlyTyrThrIleUryPheIleProIleAspIleLeuAsp 60
 Db 121 CCTTGGCTCAACATAACGGCTAACCTTAAGTTCCTCCGGAGGATTAATAGAC 180
 QY 61 LeuValIleGlyIleAlaSerIlePheIleLeuIleGlyIleIleGlyThrSerTyrHis 80
 Db 181 CTCTTAAGGGCATCGGGAGTACGGTACAGTATAGAGATAACGGAGGACTACGGAC 240
 QY 81 AlanIleLeuProLeuIleProLeuIleSerArgValGluIleAlaGlnValGlnArgAspArgIle 100
 Db 241 GCAATCTCCCTCTCCCTGAGCTTCAGCAGTGGAGCAGAGCTTGAGGATAGGGAA 300
 QY 101 ValIleGluIleLeuIlePheIleLeuIleSerProIleGlyPheIleProIleLeuIleTyr 120
 Db 301 GTTAAGGAGAGCTCTGAGCTCTCCAGGATTCGCTCCAGAGCTCGCTCCAGAGCTCGCTAT 360
 QY 121 AspProlleIleProAlaIleLeuIleAspDnsArgGlyIleArgIleGlyLeuPheAlaAspGly 140
 Db 361 GACCGATATCCCTGCACTAGCTGAGGACACGTTTACGATCTGGCCAGGG 420
 QY 141 GluAlaMetIleUpheSerAlaHisLeuAsnSerAlaIlePheAspIleProLeuIleTyr 160
 Db 421 GAGGGATGCTTCTCAGCTCATCTCACTCGGATATAAGCCATTAAACCGCTCAT 480
 QY 161 ProIleIleLeuIlePheSerAlaHisLeuAsnSerAlaIlePheAspIleProLeuIleTyr 180
 Db 481 CCACACCTTAAAGGCCAAAGGAAAGGCTTTAGGTACATCAGCTATCTCTCTGT 540
 QY 181 LeuArgGluIleLeuIleGlyIleAlaIleIleLeuIlePheArgGlyIleValIleLeuIle 200
 Db 541 CTCAAGGAGCTTAAAGCTAAAGCTAAAGCTAAAGCTGTTTGGAGGTAGGTAAAGCA 600
 QY 201 ValIysAspIleGluIalavalProvalTrpIalavalAsnThrAlaIleIle 220
 Db 601 GTCAAGACATCGAGCCCTACCCGGTTGGCTGGCGTCAACACGGCTGTAATGCTCGC 660
 Db 221 IleGlyArgLeuProLeuMetAspProlyIleValIleGluIleGlyIleValIleLeuIle 600
 Db 661 ATCGGAAGGCTCTCTTATGAACTCTAGAACTGAACTGCGCTAGAGCAGCTGATAGGAC 720
 QY 241 AsnIleLeuLeuIleUryGlyThrAspIleLeuIleGluIleGlyIleGlyTyr 260
 Db 721 AACATTCCTCTATAGGACCGTTAGAGCTTAAAGCTCTGGCTATAAGGACTTGGCCT 780
 QY 261 ArgMetSerValGluGlyLeuIleLeuIleAspIleLeuIleSerIlePheIleAsp 280
 Db 781 AGATGAGTGTGAGGATTAAGGTATAGACGAGCTACCTGGCTATAGGACTTGGCCT 840
 QY 281 ProSerGluLeuIleIshisArgIleGlyLeuIleLeuIleGluLeuAsnSerGluLeu 280
 Db 841 CCCCTAGAGCTGAACACAGCTGGAGGAGCTACGGCTACGGCTAC 900
 QY 301 AspIleSerLeuIleArgIleIlePheAspIleGluIleAsnAlaArgLeuAsnMetLeu 320
 Db 901 GATAGAGCTTAAAGCTTAAAGCTCTGGCTATAGGACTTGGCCT 960
 QY 321 TyrAsnMetArgGlyGluIleIlePheIleAlaGluAsnSerAspIleArgGlyIle 340
 Db 961 TACATATAGGAGCTGAGCTCCCTTCTAGCGAGACAGCTGATGCGAGGAGCTGGAG 1020
 QY 341 ProLeuProGluArgArgLeuAspIlePheArgAlaIleTyrAsnAspIleArgGlyIle 360
 Db 1021 CCCCTCCCTGAGGAGGCTGATGCCCTCCGGCGATATAAGCTGTTGGGGGIGAA 1080

QY 361 AspGlyGluPro 364
 Db 1081 ATGGGGAACT 1092

;

LOCATION: (1)...(1092)

us-10-112-331-3

Alignment Scores:

Pred. No.:	2.56e-208	Length:	1095
Score:	1870.00	Matches:	362
Percent Similarity:	99.73%	Conservative:	1
Best Local Similarity:	99.45%	Mismatches:	1
Query Match:	99.52%	Indels:	0
DB:	13	Gaps:	0

US-09-886-400A-4 (1-364) x US-10-112-331-3 (1-1095)

QY 1 LeuArgAlaLeuValPheHisGlyAsnLeuGlnTyraLeuAlaGluLeuProLysGluLeu 20

Db 1 TTGAGAGCCTCGTCCTTACGGAACTCCAGTATGCCAGAACGAGAACGAGCTTAATGCTGCC 60

QY 21 ProLySValLeuGluLeuValTyreProValLeuGluLeuProLysGluLeu 40

Db 61 CCAAGGTCATAGAGAACATACATCCCGATCCAGAACGAGAACGAGCTTAATGCTGCC 60

QY 41 ProPheGlyLeuAsnLeuThrGlyTyrThrLeuLysPheLeuProLysAspLeuLeuAsp 60

Db 121 CCTTTGGCTCACATAGGGCTATACCTAAAGTCTCCCGAGGATATAAGTGGAGGGGAA 180

QY 81 AlaLeuLeuProLeuLeuProLeuSerProValGluAlaGlnValNArgAspGlu 100

Db 241 GCAATACTCCCTCCCTCCGCTTAGAGTAGAGAACGAGATATCCGACAGACAGCAC 240

QY 101 ValysGluGluLeuPheGluValSerProLysPheProLeuProLeuAlaTyr 120

Db 301 GTTAAAGGAGAGCTTCAGCTTCTCAAAAGGATCTGGCTGCCAGACGCTCC 360

QY 121 AspProLeuLeProAlaLeuLeuLysAspAsnGlyTyrGluTyreLeuLeuAlaAspGly 140

Db 361 GACCAGATATCCCTGCCATACAGAGGAAACGGTTAGAGTACATTCGCGACGG 420

QY 141 GluAlaMetLeuPheSerAlaHisLeuAsnSerAlaLeuAsnSerAlaLeuProLeuAla 160

Db 421 GAGGGATGCTTCTCAGCTCACATCGGGATAAGCAATTAAACGGCT 480

QY 161 ProHisLeuLeuLeuAlaGlnArgGluLysArgPheAspGlyTyrLeuSerTyraLeuLeu 180

Db 481 CCACACTTAAAGGCCAAAGGAAAGCGCTTACGCTCATCTCCTGGT 540

QY 181 LeuArgGluLeuArgLysAlaLeuLysLeuValPheGluGlyLysValThrLeuLysAla 200

Db 541 CTCAAGGACTCTAGAGGACATAAGCGTATTCGAGTAGAGCTAACGCA 600

QY 201 ValysAspLeuGluAlaValAlaProValTrpValAlaValAlaThrAlaValMetLeuGly 220

Db 601 GTCAAGAGCTCGAGCGTACCGTTGGTGGCCGTCACAGGCTTAATGCTGCC 660

QY 221 IleGlyArgLeuProLeuMetAspProLysLysAlaSerTrpIleGluAsp 240

Db 661 ATCGGAAGCTTCCTCTTAAAGCTTACGAACTGGCTAGGGCAAGGCAAGGC 720

QY 241 AsnLeuLeuLeuTyrGlyThrAspLeuPheIleGlyTyrAspLeuLeuAla 260

Db 721 AACATCTCTTATCGGACCGATATAGGCTCTGCTGATAGGCTACGGCTAC 780

QY 261 ArgMetSerValGluGlyLeuLeuLeuIleGluValIleAspGluLeuAsnSerLeuCysLeu 280

Db 781 AGATGAGAGCTTGAGGATTATAGGGTTATAGGCTACGAGCTCACTCGGAAC 840

QY 281 ProSerGluLeuLeuHisArgGlyLeuLeuTyrLeuArgThrSerSerTrpAlaPro 300

Db 841 CCCTGAGAGCTGAGCACACTGGAGGAGCTCTTACGGACTTCGAGTTGGCACCA 900

;

RESULT 7

US-10-112-377-3

;

Sequence 3, Application US/10112377

;

Publication No. US200201201081

;

GENERAL INFORMATION:

;

APPLICANT: DIVERSA CORPORATION

;

APPLICANT: Murphy, Dennis

;

APPLICANT: Ried, John

;

TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE

;

FILE REFERENCE: DIVER1120-4

;

CURRENT APPLICATION NUMBER: US/10/112-377

;

PRIOR APPLICATION NUMBER: 09/886, 400

;

PRIOR FILING DATE: 2001-06-20

;

PRIOR APPLICATION NUMBER: 09/619, 032

;

PRIOR FILING DATE: 2000-07-19

;

PRIOR APPLICATION NUMBER: 09/407, 806

;

PRIOR FILING DATE: 1999-09-20

;

PRIOR APPLICATION NUMBER: 08/613, 220

;

PRIOR FILING DATE: 1996-03-08

;

NUMBER OF SEQ ID NOS: 4

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 1095

;

TYPE: DNA

;

ORGANISM: Thernococcus alcaliphilus

;

FEATURE: CDS

;

NAME/KEY: CDS

;

LOCATION: (1)...(1092)

;

US-10-112-377-3

;

Alignment Scores:

Pred. No.:	2.56e-08	Length:	1095
Score:	1870.00	Matches:	362
Percent Similarity:	99.73%	Conservative:	1
Best Local Similarity:	99.45%	Mismatches:	1
Query Match:	99.52%	Indels:	0
DB:	13	Gaps:	0

US-09-886-400A-4 (1-364) x US-10-112-377-3 (1-1095)

QY 1 LeuArgAlaLeuValPheHisGlyAsnLeuGlnTyraLeuAlaGluLeuProLysGluLeu 20

Db 1 TTGAGAGCCTCCTCTCACGCAACTCCAGTATGCCAGAACGAGCTTAATGCTGCC 60

QY 21 ProLySValLeuGluLeuValTyreProValLeuGluLeuLeuAsp 40

Db 61 CCAAGGTCATAGAGAACATACATCCCGATCCAGAACGAGCTTAATGCTGCC 60

QY 41 ProPheGlyLeuAsnLeuThrGlyTyrThrLeuLysPheLeuProLysAspLeuLeuAsp 60

Db 121 CCTTTGGCTCACATACGGCTATCCAGTATGCCAGAACGAGCTTAATGCTGCC 180

QY 61 LeuValysGlyGlyLeuAsnLeuAspLeuLeuLeuGluLeuLeuGlyTyrSerTyrrHis 80

Db 181 CTCCTTAAGGGGCACTGGCAACTGAGCTGAGTATGGAGGAGCTACCGAC 240

PRIOR APPLICATION NUMBER: 09/886,400
 PRIORITY FILING DATE: 2001-06-20
 PRIORITY APPLICATION NUMBER: 09/619,032
 PRIORITY FILING DATE: 2000-07-19
 PRIORITY APPLICATION NUMBER: 09/07,806
 PRIORITY FILING DATE: 1999-09-20
 PRIORITY APPLICATION NUMBER: 08/613,220
 PRIORITY FILING DATE: 1996-03-08
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 1095
 TYPE: DNA
 ORGANISM: Thermococcus alcaliphilus
 FEATURE: CDS
 LOCATION: (1)...(1092)
 US-10-116-581-3
 Alignment Scores:
 Pred. No.: 2.56e-208
 Score: 1870.00
 Percent Similarity: 99.73%
 Best Local Similarity: 99.45%
 Query Match: 99.52%
 DB: 13
 Gaps: 0
 US-09-886-4001-4 (1-364) x US-10-116-581-3 (1-1095)
 Qy 1 Leu Arg Gln Leu Val Phe His Gln Asn Ile Gln Val Thr Leu Ile Asp 200
 Db 1 TTGAGGCGCTCGTCTTCAGGGCACCTTCAGCTATGGCTATGGCACATGGCTAC 60
 Qy 21 Pro Leu Val Leu Gln Ile Asp Leu Val Ile Pro Val Leu Glu Thr Leu Ile Asp 200
 Db 61 CCAAGGTCTAGAGAAGGCATACATCCAGTCATGAGACACTGATTAAGGAATT 120
 Qy 41 Pro Phe Gln Ile Asn Ile Arg Gln Val Asp Leu Val Ile Pro Leu Asp Ile Asp 60
 Db 121 CCTTTGGCTCAQATANGGCTATACCTATAGTTCTCCGAGGATATATAGAC 180
 Qy 61 Leu Val Leu Gln Ile Asp Asp Leu Val Ile Pro Val Leu Glu Thr Leu Ile Asp 80
 Db 61 CCAAGGTCTAGAGAAGGCATACATCCAGTCATGAGACACTGATTAAGGAATT 120
 Qy 41 Pro Phe Gln Ile Asn Ile Arg Gln Val Asp Leu Val Ile Pro Leu Asp Ile Asp 60
 Db 121 CCTTTGGCTCAQATANGGCTATACCTATAGTTCTCCGAGGATATATAGAC 180
 Qy 81 Ala Leu Leu Pro Leu Leu Pro Leu Ser Arg Val Glu Leu Val Gln Arg Asp Arg Glu 100
 Db 121 GCAATACTCCCCCTCCCGCTTAGCAGAGTAGAGACAGTCAGAGATAGGA 300
 Qy 101 Val Leu Gln Leu Val Phe Gln Asp Leu Val Ile Pro Val Leu Glu Thr Leu Ile Asp 120
 Db 301 GTTAAGGAAAGGCGCTTCGAGCTTCAGGGATTCGCTCCAGGCTCAT 360
 Qy 121 Asp Pro Ile Pro Ala Leu Ile Asp Asp Asp Gln Val Val Gln Arg Asp Arg Glu 140
 Db 361 GACCGATATCCCTGCCATATCTAGAGGACACCGTTAGAGATCTATTCGCC 420
 Qy 141 Glu Ala Met Leu Phe Ser Ala Ile Leu Ile Asp Asp Gln Val Val Gln Arg Asp Arg Glu 160
 Db 421 GAGGGATGCTTCCTCAGCTCACTCGCGATAAGCCATTAAACCCCTAT 480
 Qy 161 Pro His Leu Ile Val Asp Leu Val Ile Pro Leu Val Ile Pro Leu Val Ile Asp 180
 Db 481 CCACACTTATAGGCCAAAGGAAAGGCCCTTGGCTATAGCTATCTCTGGT 540
 Qy 181 Leu Arg Gln Leu Arg Lys Ile Asp Leu Val Phe Gln Gln Asp Gln Val Val Gln Arg Asp Arg Glu 160
 Db 541 CTCAGGGAGCTTAGAGAGGATAAGCTCGTCTTGAAGGTTAGGTAACGCTAAAGCA 600
 Qy 181 Leu Arg Gln Leu Arg Lys Ile Asp Leu Val Phe Gln Gln Asp Gln Val Val Gln Arg Asp Arg Glu 160
 Db 541 CTCAGGGAGCTTAGAGAGGATAAGCTCGTCTTGAAGGTTAGGTAACGCTAAAGCA 600
 Qy 201 Val Ile Asp Ile Gln Val Val Pro Val Val Val Val Val Val Val Met Leu Ile Asp 220
 Db 601 GTCAAGAGCATCGAGCCCTACCGGTTGGTGGCGCTGAGACAGCTGCTAATCTCGGC 660
 Qy 221 Ile Gln Yarg Leu Pro Leu Met Asp Pro Ile Val Pro Leu Val Ile Asp Leu Val Ile Asp 240
 Db 661 ATGGAGGAGCTCTCTCTTATGAATCTAGCTAGCTAGGCTATGGCGCTGGCTAGGGAC 720
 Qy 241 Asp Ile Leu Leu Tyr Gln Ile Asp Ile Gln Val Phe Ile Gln Asp Gln Asp Ile Arg Gln Val Val 260
 Db 721 AACATTCCTTATAGGGCACCGATATAGCTTCATGGCTATAGGACATGCGAGCTAC 780
 Qy 261 Arg Met Ser Val Gln Gln Ile Leu Val Ile Asp Gln Leu Asn Ser Gln Leu Cys Leu 280
 Db 781 AGAATGAGCTGTGAGGGTTATAGAGGTATAGAGCTCACTCGGACTCTGCCT 840
 Qy 281 Pro Ser Gln Leu Ile Val Ile Gln Asp Gln Val Val Ile Pro Val Leu Gln Ile Asp 300
 Db 841 CCTCTGAGCTGTGAGCTGAGCTGGAGGGAGCTACTAGGGATTCTGAGTTGGCCACCA 900
 Qy 301 Asp Ile Ser Leu Arg Ile Pro Ile Val Phe Gln Asp Gln Asp Ile Asp 320
 Db 901 GATAGAGCTTGAGGATATGAGAGGAGGAGGAGGAGGAGGAGCTTAAATGCTGTC 960
 Qy 321 Tyr Asn Met Arg Gln Glu Leu Val Ile Asp Ser Asp Phe Val Ile Arg Gln Val Val 340
 Db 961 TACATATGAGGGCGGAACCTGCCTTTAGCCGGAACAGCGATGCAAGGGATGGG 1020
 Qy 341 Pro Leu Pro Gln Val Ile Val Asp Ile Asp Ile Arg Asn Ile Tyr Asn Asp Ile Asp Gln Val Val 360
 Db 1021 CCCCTCCCTGAGGAGGCTCCCTCGGGAGGATATAGGATGGGGGTGAA 1080
 Qy 361 Asp Gly Glu Pro 364
 Db 1081 AATGGGGAACT 1092
 RESULT 8
 US-10-116-581-3
 Sequence 3: Application US/10116581
 Publication No. US2002137116A1
 GENERAL INFORMATION:
 APPLICANT: DIVERSA CORPORATION
 APPLICANT: Murphy, Dennis
 APPLICANT: Reed, John
 TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND
 FILE REFERENCE: DIVER1120-4
 CURRENT APPLICATION NUMBER: US/10/116, 581
 CURRENT FILING DATE: 2001-04-03

Db 1081 AATGGGGAACT 1092 Qy 141 GluAlaMetLeuPheSerAlaHisLeuAsnSerAlaIleLeuProLeuIleProLeuTyr 160
 RESULT 10 Db 421 GAGGGCATGCTTTCAGTCATCTCACTGGCGATAAGCCATAACGGCTTAT 480
 ; Sequence 3, Application US/10112418
 ; Publication No. US2002015548A1 Qy 161 ProHisLeuIleLeuAlaGlnArgIleIleArgPheArgTyrIleSerTyrLeuIleGly 180
 ; GENERAL INFORMATION: Db 481 CCACTCTTAAGGCCAGGGAAACGGCTTACGGTACATGCTAATCTCTTGT 540
 ; APPLICANT: DIVERSA CORPORATION Qy 181 LeuArgGluLeuAglGlySerAlaIleLeuValPheGlyIleLeuValTyrLeuIleAla 200
 ; APPLICANT: Murphy, Dennis Db 541 CTCAGGGAGCTTAGGAGGGATAAGCTGTTTGAAGGTAAGCTAACGGCA 600
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: DIVER1120-4
 ; CURRENT APPLICATION NUMBER: US/10/112,418
 ; CURRENT FILING DATE: 2002-03-29
 ; PRIOR APPLICATION NUMBER: 09/886,400
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 09/619,032
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/497,806
 ; PRIOR APPLICATION NUMBER: 08/613,220
 ; PRIOR FILING DATE: 1996-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq For Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 1095
 ; TYPE: DNA: Thernococcus alcaliphilus
 ; FEATURE: CDS
 ; NAME/KEY: CDS
 ; LOCATION: (1) ... (1092)
 ; US-10-112-418-3
 Alignment Scores:
 Pred. No.: 2. 566-208 Qy 201 VallyLeuAspIleGluIleAlaValProValTrpValAlaValAlaValAlaValMetIleGly 220
 Score: 1870.00 Length: 1095
 Percent Similarity: 99.73% Matches: 362
 Best Local Similarity: 99.45% Conservative: 1
 Query Match: 99.52% Mismatches: 1
 DB: 13 Indexes: 0
 Gaps: 0
 US-09-886-400A-4 (1-364) x US-10-112-418-3 (1-1095)
 Qy 1 LeuArgGalaLeuIlePheHisGlyValLeuGlnIlePheLeuIleProLeuSerGluIle 20
 Db 1 TTGACAGCGCTGCTGCTTCAAGCCACTTCAGATGCCAAATCCAAAGGGAAATC 60 Qy 361 AspGlyGluPro 364
 Qy 21 ProlyValIleGluIleAlaTyrIleProValLeuGluIleLeuAlaGluAsnSerAlaIle 40
 Db 61 CCAAGGTCCTAGAGGAGATACCCCTCATGAGCACTTAAAGAAATT 120 Db 1021 CCCCCTCTGAGGGCTGAGCTGATCTCCAGGATATAGAGCTGAA 1080
 Qy 41 ProheGlyLeuAsnIleIleGlyTyrIleIleLeuProLeuSerGlyAspIleLeuPhe 60 Qy 321 TyrAspMetArgGlyGluLeuAlaPheLeuAlaGluAsnSerGlyAspIleLeuSer 320
 Db 961 TACATATGAGGGCGACCTGCCCTTACGCCAGACAGGATGCAAGGGGTGGAG 1020 Db 901 GATAAGAGCTTGGAGGATATGGAGAGGAGGAAAGCAAGACTTATATGCTGTC 960
 Db 341 ProLeuProGluIleGluGlyAspIleLeuAspAlaPheArgAlaIleTyrAsnAspIleArgIleGlu 360
 Db 321 TyrAspMetArgGlyGluLeuAlaPheLeuAlaGluAsnSerGlyAspIleLeuSer 320
 Db 961 TACATATGAGGGCGACCTGCCCTTACGCCAGACAGGATGCAAGGGGTGGAG 1020
 Db 1021 CCCCCTCTGAGGGCTGAGCTGATCTCCAGGATATAGAGCTGAA 1080
 Qy 361 AspGlyGluPro 364
 Db 1081 AATGGGGAACT 1092 Qy 141 GluAlaMetLeuPheSerAlaHisLeuAsnSerAlaIleLeuProLeuIleProLeuTyr 160
 RESULT 11 Db 421 GAGGGCATGCTTTCAGTCATCTCACTGGCGATAAGCCATAACGGCTTAT 480
 ; Sequence 3, Application US/10114083
 ; Publication No. US20020160464A1 Qy 161 ProHisLeuIleLeuAlaGlnArgIleIleArgPheArgTyrIleSerTyrLeuIleGly 180
 ; GENERAL INFORMATION: Db 481 CCACTCTTAAGGCCAGGGAAACGGCTTACGGTACATGCTAATCTCTTGT 540
 ; APPLICANT: DIVERSA CORPORATION Qy 181 LeuArgGluLeuAglGlySerAlaIleLeuValPheGlyIleLeuValTyrLeuIleAla 200
 ; APPLICANT: Murphy, Dennis Db 541 CTCAGGGAGCTTAGGAGGGATAAGCTGTTTGAAGGTAAGCTAACGGCA 600
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: DIVER1120-4
 ; CURRENT APPLICATION NUMBER: US/10/114,083
 ; CURRENT FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: 09/886,400
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 09/619,032
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/407,806
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 08/613,220
 ; PRIOR FILING DATE: 1996-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq For Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 1095

Alignment Scores: 2.56e-208 Length: 1095
 Pred. No.: 1870.00 Matches: 362
 Score: 99.73% Conservative: 1
 Percent Similarity: 99.45% Mismatches: 1
 Best Local Similarity: 99.52% Indels: 0
 Query Match: 13 Gaps: 0

US-09-886-400a-4 (1-364) x US-10-114-083-3 (1-1095)

Qy 1 LeuArgAlaLeuAlaValPheHisGlyAsnLeuGlnTrpAlaGluLeuProLeuSerGluLe 20
 Db 1 TTGAGAGGGCTCGCTTCAAGCACAACCTCACTATCCGAATCCGAAAGGAGCAATC 60

Qy 21 ProlysValLeuGluLysAlaTyrIleProValLeuGluThrIleLeuIleGluGluLe 40
 Db 61 CCAAGGCTTAAAGGCTTACAGGCAACTTCAGTATCCGAACTGAGAACTGATTAAGAATT 120

Qy 41 PropheGlyLeuAsnIleThrGlyTyrThrLeuIysPheLeuProLeuAspIleLeuAsp 60
 Db 121 CCTTGTGGCTCAACATAAGGGCTATACCTTAAGTCTCCGAAAGGATATTAGAC 180

Qy 61 LeuValIleGlyGlyIleLeuSerAspIleLeuIleLeuIleGlyThr-SerThrHis 80
 Db 181 CTCGTTAAAGGGGCTCAGCAGTACGAGTACGATAGAGATTCGAAACGAGCTACGGAC 240

Qy 81 AlanLeuLeuProLeuLeuProLeuSerArgValGluAlaGlnValGlnArgAspArgL 100
 Db 241 GCATTAATCCCCCTCCGGCTAGAGTAGAGAGAGAGCAACGAGAGATAGGAA 300

Qy 101 ValysGluGluLeuPheGluValSerProlysGlyPhePheProGluLeuLeuAlaTyr 120
 Db 301 GTTAAAGGAAAGCTCTTCGCTTCCTCCAAAGGGATTCTGGCAGCTGGCCAT 360

Qy 121 AspProLeuLeuProAlanLeuLeuIysAspAlaGlyTyrGlyIleLeuLeuAlaAspGly 140
 Db 361 GACCGGATATCCCTGGCTTCACTGAGGACACGTTATGAGTAATCTTCGGACCGG 420

Qy 141 GluAlaMetLeuLeuSerAlaHisLeuAsnSerAlaIleLeuIleProIysProLeuTyr 160
 Db 421 GAGGGATCTTCTCTGACTCTCACTCTCAACTCTCGCGATTAAGCAATTAAACGGCTCTAT 480

Qy 161 ProHisLeuIleLeuAlaIleGlnArgGluIysBargPheArgTyrIleSerTyrLeuLeuGly 180
 Db 481 CCACACTTAAAGGCCAAAGGAAACGCCGTTAGGTTACATCAGCTACCTCTGT 540

Qy 181 LeuArgGluLeuArgIysAlaIleLeuIleLeuValPheGluGlyIleLeuValThrLeuIysAla 200
 Db 541 CTCAGGGAGCTTACGGAGGCTAACGCTGTTGAGGTAGGTAAAGGCA 600

Qy 201 ValysAspIleGluAlaValProValTyrValAlaValAsnThrAlaValMetLeuGly 220
 Db 601 GTCAAAGACTCTGAAAGCCGTACCCCTTCTGCT 650

Qy 221 IleGlyArgLeuProLeuMetAsnProIysValAlaSerTyrIleGluAspIysAsp 240
 Db 661 ATCGGAGGTTCCTCTTCTGAAAGGAAAGGGCTAGGCTAAGGAGAC 720

Qy 241 AsnIleLeuLeuIleGlyIleLeuAspIleGluIleLeuIleGlyIleArgAspIleAlaGlyTyr 260
 Db 721 AACATCTCTTATACGGACCGATATAGGTTATGGCTATAGGGACATTCGAGCTAC 780

Qy 261 ArgMetSerValGluIleLeuLeuIleAspIleGluLeuAsnSerGluLeuCysteau 280
 Db 781 AGATCTAGTGTGAGGATTTAGGGTTATAGGGAGTCACCTGGACTCTGGCTT 840

Qy 281 ProSerGluLeuIleIleIleGlyArgGluLeuTyrIleIleGlyArgSerSerTtpAlaPro 300
 Db 841 CCCTCAGGAGCTGAAAGCAGCAGGAGCTACTAGGACTCTGAGTTGCGACCA 900

Qy 301 AspIysSerLeuArgIleTtpArgGluAspGluIysAlaArgLeuAsnMetLeuSer 320
 Db 901 GATAAGGCTTGAGGAATGGAGGAGCAAGGAAAGCAACTTATATGTGTC 960

Qy 321 TYRASDMEArgGlyIleLeuAlaPheLeuAlaGluAsnSerAspAlaArgGlyTyrGlu 340
 Db 961 TACAATATGAGGGGCAACTCGCCCTTTAGCCGAGACACGATCAGGGATGGGAG 1020

Qy 341 ProLeuProGluIargArgLeuAspAlaPheArgAlaLeuIleTyrAspItpPArgGlyGlu 360
 Db 1021 CCCTCCTGAGGAGGCTGATGCCTTCGGGCGATAATAACGATTCGAGGAGCTGAA 1080

Qy 361 AsnGlyGluPro 364
 Db 1081 ATGGGGGAACT 1092

RESULT 12 US-10-282-122A-17097

; Sequence 17097, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA_034A
 ; CURRENT APPLICATION NUMBER: US/10/282-122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 200-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 17097
 ; LENGTH: 2670
 ; TYPE: DNA
 ; ORGANISM: Clostridium difficile
 ; US-10-282-122A-17097
 ; Alignment Scores: 0.0446 Length: 2670
 ; Pred. No.: 111.50 Matches: 72

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 28, 2005, 02:20:58 ; Search time 109 Seconds

(without alignments)

2373.641 Million cell updates/sec

Title: US-09-886-400A-4

Perfect score: 1879

Sequence: 1 LRALVFGHNLQYAEIPKSEI.....RRLDAFRAIYNDWRGNGEPE 364

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 1.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODBL=frame+p2n.model -DEV=x1p
-Q=cgn2_1/USP10_spool/p1US0986400/runat 27012005 055722 17947/app query fasta_1.519
-DB=cgn2_1/USP10_spool/p1US0986400/runat 27012005 055722 17947/app query fasta_1.519
-LOOPEXT=0 -UNITS=5tb -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cai
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=PTO -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER US0986400@CGN_1.1_105 @runat 27012005 055722 17947 -NCPP=6 -ICPU=3
-NO NMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:
1: /cgn2_6/pctdata/1/ina/5a_COMB.seq:
2: /cgn2_6/prodata/1/ina/5b_COMB.seq:
3: /cgn2_6/prodata/1/ina/6a_COMB.seq:
4: /cgn2_6/pctdata/1/ina/6b_COMB.seq:
5: /cgn2_6/prodata/1/ina/pcrtrs_COMB.seq:
6: /cgn2_6/prodata/1/ina/backfilesl.seq:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	
1	1879	100.0	1095	4 US-10-166-06-3	
2	100.0	1095	4 US-10-166-06-3	Sequence 3, Appli	
3	1589	84.6	1041	2 US-08-613-220B-3	Sequence 3, Appli
4	146.5	7.8	164976	4 US-08-916-421B-1	Sequence 1, Appli
5	140.5	7.5	3139	1 US-07-894-212A-1	Sequence 1, Appli
6	105	5.6	684	4 US-09-107-332A-1900	Sequence 1, Appli
7	104	5.5	4403765	3 US-09-103-840A-2	Sequence 2, Appli
8	104	5.5	4411529	3 US-09-103-840A-1	Sequence 1, Appli
9	103	5.5	5030	4 US-08-956-171E-324	Sequence 3,24, Appli
10	5.5	5030	4 US-08-781-886A-24	Sequence 1, Appli	
11	102.5	1912	1 US-08-270-013B-1	Sequence 1, Appli	
12					

RESULT 1

US-10-166-606-3

; Sequence 3, Application US/10166606
; Patent No. 6644756
; GENERAL INFORMATION:
; APPLICANT: Murphy, Dennis
; APPLICANT: Reid, John
; TITLE OF INVENTION: ALPHA GALACTOSIDASES AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING THEM (Amended)
; FILE REFERENCE: 09010-000405
; CURRENT APPLICATION NUMBER: US/10/166,606
; CURRENT FILING DATE: 2003-01-31
; PRIORITY APPLICATION NUMBER: US 09/407,806
; PRIORITY FILING DATE: 1999-09-28
; PRIORITY APPLICATION NUMBER: US 08/613,220
; PRIORITY FILING DATE: 1996-03-08
; NUMBER OF SEQ ID: NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Thermococcus alcaliphilus
US-10-166-606-3

Alignment Scores: 1.16e-230

Length: 1095

Score: 1879.00

Matches: 364

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Mismatches: 0

Gaps: 0

Indels: 0

Query Match: 4

DB:

QY 1 LeuArgAlaLeuValPheIleGlyAsnLeuGlnPheIlePheGlySerGlyle 20

RESULT 2
US-10-112-231A-3
; Sequence 3, Application US/10112231A
; Patent No. 6744246
; GENERAL INFORMATION:
; APPLICANT: Murphy, Dennis
; APPLICANT: Reid, John
; TITLE OF INVENTION: ALPHA GALACTOSIDASES AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING THEM (Amended)
; FILE REFERENCE: 09010-004005
; CURRENT APPLICATION NUMBER: US/10/112.231A
; CURRENT FILING DATE: 2002-03-29
; PRIORITY NUMBER: US 09/407,806
; PRIORITY NUMBER: US 08/613,220
; PRIORITY FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Thermococcus alcaliphilus
US-10-112-231A-3

Alignment Scores:
Pred. No.: 1.16e-230 Length: 1095
Score: 1879.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Query Match: 100.00% Mismatches: 0
DB: 4 Indels: 0
Gaps: 0

US-09-886-400A-4 (1-364) x US-10-112-231A-3 (1-1095)

QY 1 Leu Arg Glu Leu Val Phe His Gly Asn Leu Ile Thr Ala Glu Leu Pro Ile Ser Glu Ile 20
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DB 601 GTCAAAGAACATCGAGCCCTACCGCTTGGTGGCCGTCACAGGCTGTAAATGCTCGC 660
QY 221 Ile Glu Arg Leu Pro Leu Leu Asn Pro Val Pro Val Val Leu Ile Asn Leu Ile Asn Leu Ile 240
DB 661 ATCGAGACCTCTCTCTATGAACTCTAGAAAGTGGCTGGCACTGGATAGAACGAC 720
QY 241 Asn Ile Leu Ile Asn Leu Ile 260
DB 721 AACATCTCTTATAGGCACGATATAGGACATTCAGGTAC 780
QY 261 Arg Met Ser Val Glu Glu Leu Leu Ile Asp Glu Leu Ile Asn Ser Glu Leu Ile Asn Leu Ile 280
DB 781 AGATGAGCTGTGGGGATTATAGGACGCTTACCTGGCTT 840
QY 281 Pro Ser Glu Leu Ile Asn 300
DB 841 CCTCTGAGCTGAAAGACAGCTGGAGGAGCTCTACTGGACTTGAGTGGGACCA 900
QY 301 Asp Lys Ser Leu Arg Ile Trp Arg Glu Asp Glu Gly Ile Asn Asp Arg Leu Asn Met Leu Ser 320
DB 901 GATAGAGCTTGAGGATGAGAGAGCTGGAGGAGCAAGCTTAATGCTCC 960
QY 321 Tyr Asp Met Arg Gly Glu Leu Ile Asp Leu Ile Asn Ser Asp Asp Leu Ile Asn Ser Asp Asp 340
DB 961 TACATATGAGGGCGCACTCGCCTTTAGCCGAGACCGATGAGGATGGAG 1020
QY 341 Pro Leu Pro Glu Arg Arg Leu Ile Asp Leu Ile Asn Ser Asp Pro Leu Ile Asn Ser Asp Asp 360
DB 1021 CCCCCTCCTGAGGAGGCTGGATGCCCTTCGCGCGATAATACGATGGAGGGTGAA 1080
QY 361 Asp Glu Glu Pro 364
.DB 1081 Asn TGGGAACT 1092

Db 685 AACATCTCTATAGGCACCGATATAGCTCATGGCATATGGACATTGAGG-... 741 ;
 Qy 261 ArgMetSerValGluGlyLeuLeuLeuLeuLeuLeuLeuLeuSerGluLeuCysLeu 280 ;
 Db 742 AGAAATGAGCTGTGAGGGATTATAGAGTTATAGACGACTCGCAACTGTC-... 798 ;
 Qy 281 ProSerGluLeuYBHissArgIArgGluLeuTyLeuArgThrSerSerTAlaPro 300 ;
 Db 799 CCCTCAGAGCTGAAGCACAGTGGAGGGAGCTCACTGAGACTCGCAACTGTC-... 855 ;
 Qy 301 AspLysSerLeuArgLeuTrpArgGluArgGluGlyAsnAlaArgLeuAsnMetLeuSer 320 ;
 Db 856 GATAAGAGCTTGAGAAATAGGAGAGGAGGAGGAAACGCCAGCTGAGCTG-... 912 ;
 Qy 321 TyrAsnMetArgGlyGluLeuAlaPheLeuAlaGluAsnSerAspAlaPheArgGlyTyrAla 340 ;
 Db 913 TACATATGAGGGGGCACTCGCCATTGAGCCAGAAGCGATGCAAGGGATGG-... 969 ;
 Qy 341 ProLeuProGluArgArgLeuAspAlaPheArgAlaLeuTyrAsnAspTrpArgGlyGlu 360 ;
 Db 970 CCCCTGCCAGAGGAGGAGCTGGATGCTTCCGGCGATATAACGATGAGGGT-- 1026 ;
 Qy 361 AspGlyGluPro 364 ;
 Db 1027 AATGGGAACCT 1038 ;
 RESULT 4 ;
 US-08-916-421B-1/C ;
 ; Sequence 1, Application US/08916421B ;
 ; Patent No. 6503729 ;
 ; GENERAL INFORMATION: ;
 ; APPLICANT: Bult et al. ;
 ; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ- ;
 ; Patent No. 6503729 ;
 ; FILE REFERENCE: PB2/5 ;
 ; CURRENT APPLICATION NUMBER: US/08/916,421B ;
 ; PRIOR APPLICATION NUMBER: US 60/024,428 ;
 ; PRIORITY FILING DATE: 1997-09-22 ;
 ; NUMBER OF SEQ ID NOS: 3 ;
 ; SOFTWARE: PatentIn version 3.1 ;
 ; SEQ ID NO 1 ;
 ; LENGTH: 164976 ;
 ; TYPE: DNA ;
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US-08-916-421B-1
Alignment Scores:
Pred. No.: 0.00235 Length: 1664976
Score: 146.50 Matches: 87
Percent Similarity: 40.58% Conservative: 66
Best Local Similarity: 23.08% Mismatches: 129
Query Match: 7.80% Indels: 95
DB: 4 Gaps: 24
US-09-886-400A-4 (1-364) x US-08-916-421B-1 (1-1664976)
QY 14 GlurleProlyserGluileProlyValleGluysAlaTyrileProvalleGlu 33
Db 1550943 MATTATAATAGAAGTTTATAAGTGGCTAAATATGCTACTTCCTCAAATGAG 1550784
QY 49 TyrThrLeuLysPheLeuProlysASP--IleLeuPheLeuVallySgly 64
Db 1550723 TTGTTAGGCAACCTTGGATT-----ANTGATACGTTGGATTATTTAGAT 1550670
QY 65 GlyleIleLaserAspIleIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu 84
Db 1550669 TTGTTAAACACTGGCAATGTTAGTTAGTTAGTTAGTGAACATATCATCTACTAACAGT 1550610
QY 85 LeuLeuProLeu--SerArgValGluAlaGlnValGlnArgGluVallySgly 103
Db 1550609 ATGTCAAAGATGCAAAAGATTAGCTGTTAACGCCATATTCATCACTACTAACAGT 1550550
QY 104 GluIlePheGluValSerProlysGlyPheIleProlysProlysIleLeuIleLeu 123
Db 1550549 GAATATTTGGTTAACGCCAGGCTTAAAGAACTACTGCTGTTATACACACAGA 1550490
QY 124 IleProIleIleLeuIysASPArgGlyTyrGluTyreLeuPheAlaaspGly--GluAla 142
Db 1550489 ATGCAAAAGATGCAAAAGATTAGCTGTTAACGCCATATTCATCACTACTAACAGT 1550550
QY 143 MetLeuPheSerAlaHisLeuSerSerAlaIleLeuProIleLeuProIleLeuProHis 162
Db 1550429 ATCTTA----- 1550429
QY 163 LeuIleLysAlaGlnArgGluysArgPheArgTyrIleSer-----TyrLeuLeu 179
Db 1550423 -----GGCTGGAGGCTCTCCAACTATTTCACCACTCCAGATGGTTAGAAATT 1550373
QY 180 GlyLeuArgGluLeuArgIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu 199
Db 1550372 CGTTAAAGGAATTATAGCTGTTGTTGAGACATGGCTTACG-----TTT 1550328
QY 200 AlavallysAspIleGluIalavalPro-----ValTrpValAla 212
Db 1550327 TCAAGCAAGAGATGGGACCAATTACATTAAACGCTATAATGCTATTGTTAGCT 1550268
QY 213 ValAsnThrIalavalMetLeuGlyIleGlyArgLeuProLeuMetAlaProlysVal 232
Db 1550267 TCACTCTGGGGAGTTAAACATA-----TATGACTATGAGACATT 1550220
QY 233 Alaser-----TrpIleGluAspIleLeuLeuIleLeuIleLeuIleLeuIleLeu 249
Db 1550219 GAGAACATCACTGGAAAGAA-----ACTGGAATT 1550187
QY 250 GluPheIleGlyTyrIleArg-----AspIleAlaGlyTyr--ArgMetSerValGluGly 266
Db 1550186 GAGTGTGAGATATTGCTCTATAGATAGCTAGCTAGCATTTAGGTTGTTAAT 1550127
QY 267 LeuLeuGluValIleAspGluLeuIleAspSerGluLeuProSerGluLeuIleSlysHis 286
Db 1550126 GTCAGTOAGGTTGTTAGTGTAGCCAAAG----- 1550094
QY 287 SerGlyArgGluIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu 302
Db 1550093 -----GGAGAGATTAGCTGCACTGATTGCCACGATATCATGGCTGCACTGAGAGG 1550040
QY 303 SerLeuArgIleTrpArgGluAspGluGlyAlaIleArgLeuAspMetLeuSerTyrAsn 322
Db 1550039 GATGTAAGTGTGCTGTTA-----GCGAT-----AAGGTCGAAAGAAATCTGTTGAGA 1549992
QY 323 MetArgGlyGluLeuAla--PheIleLeuAlaGluAsnSerAspAlaArgGlyTrpGluPro 341
Db 1549991 MAACTAAAGATATGGTAAATTATAAGAAGAACTCACAACAAITA----- 1549944
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US-09-692-570-1/c
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Built et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus jannaschii
; Patent No. 6797466
; TITLE OF INVENTION: Jannaschii
; FILE REFERENCE: PB215C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
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COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)891-5007

FAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 1900:

SEQUENCE CHARACTERISTICS:

LENGTH: 684 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOROLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

FEATURE:

NAME/KEY: ^{mlb}GC feature

LOCATION: (B) LOCATION 1...684

SEQUENCE DESCRIPTION: SEQ ID NO: 1900:

US-09-107-532A-1900

Alignment Scores:

Pred. No.:	0.00115	Length:	684
Score:	105.00	Matches:	60
Percent Similarity:	37.90%	Conservative:	34
Best Local Similarity:	24.19%	Mismatches:	88
Query Match:	5.59%	Indels:	66
Db:	4	Gaps:	12

US-09-886-400A-4 (1-364) x US-09-107-532A-1900 (1-684)

Qy 140 GlyGluAlaMetLeuPheSerAlaHisLeuLysSerAlaLeuLysProlLeuProLeu 159

Qy 7 GGAGAAAATGATTTCATTCATGAACTGGTG----- 45

Qy 160 TyrProHisLeuLysAlaGlnArgLysArgPheArgTyrIleSerTyrLeuLeu 179

Db 46 -----TTCGGTTCATCGGTTATTTATA 69

Qy 180 GlyLeuArgGluLeuArgLys-----AlaLeu 188

Db 70 GTCGTACGTTGCTGGAGAAATCCATGTCAGAAATCACACCGTTGATTAGCTAT 129

Qy 189 LysLeuValPheGluGlyLysValThrLeuLysAlaValLysAsp----- 203

Db 130 ACGGTTGTTAGGGGATCTAGGAAATCAACCTATGATGAGATGTCGTCAGTAGGG 189

Qy 204 -----IleGluAlaValProValItpValAlaValAsnThrAlaValMetLeu---Gly 220

Db 190 CATGTCCTATTTGCGATGGCTTG-----GCGTAGTTGATTAGCTAT 234

Qy 221 IleGlyArgLeuProLeuMetAsnProLysValAlaSerTtpIleGluAspLysAsp 240

Qy 235 ATCGAACGTTATCGTCAAAAAAT---GAAAGGCTCAATGTTGGTCAGAGGCCAGCCA 291

241 AsnIleLeuLeuItpGlyThrAspIleGluPheIleGlyItpArgAspIleAlaGlyTyr 260

RESULT 8

US-09-103-840A-2

; Sequence 2, Application US/09103840A

; Patent No. 6294328

GENERAL INFORMATION:

APPLICANT: FLEISCHMAN Robert D.

APPLICANT: WHITE, Owen R.

APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

FILE REFERENCE: 24366-2007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 4403765

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

FEATURE:

OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence

US-09-103-840A-2

Alignment Scores:

Pred. No.:	3.31e+03	Length:	4403765
Score:	104.00	Matches:	76
Percent Similarity:	34.82%	Conservative:	49
Best Local Similarity:	21.17%	Mismatches:	128
Query Match:	5.53%	Indels:	106
Db:	3	Gaps:	18

US-09-886-400A-4 (1-364) x US-09-103-840A-2 (1-4403765)

Qy 61 LeuValLysGlyGlyIleAlaSerAspLeuIleGluIleIleGlySerTyrThrHis 80

Db 3386055 CTGCTCGCGCCGCTGATGAGCCGACGGCTGCTGGTGGCGCCACTGCCAC 3386114

Qy 81 AlaIleLeuProLeuProLeuProLeuUserArgValGluAlaGlnValGlnAspAspArgLys 100

Db 3386115 CGGTTCCAGCGCTGCTG-----GCACCGCCGCTGCGGAGCTGCGCG 3386156

Qy 101 ValLysGluGluLeuPheGluValSer-----ProLyGlyPheItp 114

Db 3386157 CTGGCCGAAAGGCCCTGCCGATGCTCAGTGGGCTGGGCCACGGCCAAAGGGATCTGG 3386216 ; FILE REFERENCE: 24366-20007.00
 Qy 115 LeuProGluLeuAlaTyAspProLeuProLeuLeuLeuLeuAspArgLysTyrGlu 134 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 Db 3386217 GCACCCGAATGCCATACGCCCGGGATGAGCTGACTACGCCACCGGGGTCTGT 3386276 ; CURRENT FILING DATE: 1998-06-24
 Qy 135 TyrLeuPheAlaAspGlyGluAlaMetLeuPheSerAlaHisLeuAsnSerAlaLeu--- 153 ; NUMBER OF SEQ ID NOS: 2
 Db 3386277 CACTCAGTGTCAAGGGCGG---TOCGAGACGGACACCGCGTGGC 3386324 ; SOFTWARE: Patentin Ver. 2.1
 Qy 154 LysProLe----- 156 ; SEQ ID NO: 1
 Db 3386325 CGGGGAGGGAAACCGATGAGTCGCTCGCCACTGCAAGTCACCTACCG 3386384 ; LENGTH: 4411529
 Qy 157 -----LysProLeuTyrPro---HisLeuLeuLysAlaGlnArgGluLysArg 171 ; TYPE: DNA
 Db 3386385 GTGTGGTCACCGAAATCCGGTACCCGGCAC-----GCCCTACCGCGAC----- 3386432 ; ORGANISM: Mycobacterium tuberculosis
 Qy 172 PheArgTyrIleSerTyrLeuLeuGlyLeuArgGluLeuArgLysAlaLeuLysLeuVal 191 ; OTHER INFORMATION: H37Rv
 Db 3386433 TTCCACACTACGACCACTGACCGACTCAACCGGCGAAGCTCACGGGGTAACGGT 3386492 ; US-09-103-840A-1
 Qy 192 PheGluGlyIysValThrLeuLysValAlaValLeuAspLeuGluAlaValProValTrpVal 211 ;
 Db 3386493 CGGCGGAGGCAA-----ArgGluCCTACGATCCGAGGGCTGACCCGGCCGTC 3386543 ;
 Qy 212 AlaValAsnThrAlaValMetLeuGlyIleGlyArgLeuProLeuMetAsnProLys 231 ;
 Db 3386544 GACGCCATGTTGCCGATTCGAGCCTGGCGCAATCGCTGCTC----- 3386594 ;
 Qy 232 ValAlaSerTrpIleGluAspLysAspAsnLe-----LeuLeuTyrAla 246 ;
 Db 3386595 -----GATGCGAAGCGATCGGCCGCCACCGTGTGATGCCGCC 3386636 ;
 Qy 247 ThrAspIleGluPheLeuGlyTyr----- 254 ;
 Db 3386637 TTGACACACGAGTGTGCGCACTGGGCGTACGAGGGCCCAACTGGCTGACCGGT 3386696 ;
 Qy 255 ---ArgAspIleAlaGlyIleArgMetSerValGluGlyLeuLeuGluValLeuAspGlu 273 ;
 Db 3386697 TTGGGGCTTACCGGCCGCCGGTGTGGGGGCGACCTGAGCGGATGCCGAC 3386756 ;
 Qy 274 LeuAsnSerGluLeuCysLeuProSerGluLeuLeuLysHisSerGlyArgGluLeuTyrLeu 293 ;
 Db 3386757 -----GGATTCGTCGCGACCGGGTGAATT 3386783 ;
 Qy 294 ArgThrSerSerTrpAlaProAspLysSerLeuArgIleTrpArgGluAspGluGlyAsn 313 ;
 Db 3386784 CCACCCAACTCTTGGGGATCGCGCAAGGACTGGCAGGGTGG----- 3386834 ;
 Qy 314 AlaArgLeuAsnMetLeuSerTyrAspMetArgGlyGluLeuAla----- 328 ;
 Db 3386835 AAAGTGGCCATCTGTCACAC-----AGCGAGTGTGATACCGGGTGACC 3386888 ;
 Qy 329 -----PhelLeuAlaGluAsnSerAspAlaArgGlyTyrGluProLeuProGlu 344 ;
 Db 3386889 ACCATCGACAAGGGCTGCGGCCAGACGCTCCCTGGAGCGA-----CCGGCGCTGC 3386942 ;
 Qy 345 ArgArgLeu-----AspAlaPheArgAlaLeuTyrAspAlaTrp 357 ;
 Db 3386943 GATCACGTTGCTGATCAGATCCTGGCGCAGACCTGTCACCGCTGCGACTGG 3386999 ;
 RESULT 9
 US-09-103-840A-1
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 Alignment Scores:
 Pred. No.: 3.32e+03 Length: 4411529
 Score: 104.00 Matches: 76
 Percent Similarity: 34.82% Conservative: 49
 Best Local Similarity: 21.17% Missmatches: 128
 Query Match: 5.53% Indels: 106
 DB: 3 Gaps: 18
 US-09-886-400A-4 (1-364) x US-09-103-840A-1 (1-4411529)
 Qy 61 LeuValGlyGluGlyIleAlaSerAspLeuIleGluIleLeuGlyThrSerTyrThrHis 80 ;
 Db 3390363 CTCCTGCGGCCCTGATGACGCCGGCACGGTGACTGCTGGGCCACTGTGCCAC 3390422 ;
 Qy 81 AlaLeuLeuProLeuLeuProLeuSerArgValGluAlaGlnValGlnArgAspArgGlu 100 ;
 Db 3390423 CGTTCTCAGCCGCTGCT-----GCACCGGGCTGCGGAGTGTGGC 3390464 ;
 Qy 101 ValGlyGluGlyLeuLeuAspAsnLe-----LeuLeuTyrAla 114 ;
 Db 3390465 CTCGCGCAAGGCTCGCGGCTGCGGACACCGCCGCTGGC 3390524 ;
 Qy 115 LeuProGluLeuAlaTyAspProLeuLeuProAlaLeuLeuAspArgLysTyrGlu 134 ;
 Db 3390525 GCACCCCAATGGCAATGCCCCGGGATGGGGCTGACTACGCCACCGGGGTCACT 3390584 ;
 Qy 135 TyrLeuPheAlaAspGlyGluAlaMetLeuLeuLeuAlaHisLeuAsnSerAlaLeu--- 153 ;
 Db 3390585 CACTCTCTGGCGACGCCCG-----TCGTCGACGGCGACACCGCCGCTGGC 3390632 ;
 Qy 154 LysProLe----- 156 ;
 Db 3390633 CGCGCGTGGGAAACCGATGTTGGCCCTGGGCGACTTGCAGGTCAGCTACCG 3390692 ;
 Qy 157 -----LysProLeuTyrPro---HisLeuLeuLysAlaGlnArgGluLeuTyr 171 ;
 Db 3390693 GTGTGGTACCCAAATCGGTACCCGGGAC-----GCCCTAACGGAC 3390740 ;
 Qy 172 PheArgTyrIleSerTyrLeuLeuGlyLeuArgGluLeuArgLysAlaLeuLeuVal 191 ;
 Db 3390741 TTCCACACTGAGCAACCTACCGGACTCTAACCGCCACGGTACCCGGTAAAGTG 3390800 ;
 Qy 192 PheGluGlyLysValThrLeuLysValAlaValLeuLeuAspLeuLeuLeuLeuLeu 211 ;
 Db 3390801 CGCTCGAGCA-----AAGSCACCTACGTCAGTCGACGCCGCGCTGACCGCGCGTC 3390851 ;
 Qy 212 AlaValAsnThrAlaValMetLeuGlyIleGlyLeuLeuProLeuMetAsnProLys 231 ;
 Db 3390852 GACGTCACATGTTGGCCATTGTCGAGCTGTCGCACTCGCTGCTC 3390902 ;
 Qy 232 ValAlaSerTrpIleGluAspLysAspAsnLe-----LeuLeuTyrGly 246 ;
 Db 3390903 -----GAATTCGCGACGCCATCGGCC 3390944 ;
 Qy 247 ThrAspIleGluPheLeuGlyTyr----- 254 ;
 Db 3390945 TTGACACCGAGTTGTTGGCCACTGTGGTACGAGGGCCAACTTGGCTCAACGGTA 3391004 ;
 Qy 255 ---ArgAspIleAlaGlyTyrArgMetSerValGluGlyLeuLeuGluValLeuAspGlu 273 ;
 Db 3391005 TTGGCGCTTACCCGCCGCGGTCGCGGACCTGGGACGATGCCGAC 3391064 ;

QY 274 LeuAsnSerGluLeuCysLeuProSerGluLeuIleHissArgGluLeuIleTyrLeu 293
 Db 3391065 -----GGATCTGCTGGCAACCCGGTCGATTG 3391091
 QY 294 ArgThrSerSerTrpAlaProAspLysSerLeuArgLeuIleTyrLeu 313
 Db 3391092 CCACCCAGCTCTGGGCAAGGAGCTGGAGCTGG 3391142
 QY 314 AlaArgLeuAsnMetLeuSerTyrAsnMetArgGlyGluLeuIle 328
 Db 3391143 AAGGTGCCATCTGCTGCACT 3391196
 QY 329 -----PheLeuAlaGluAsnSerAspAlaArgGlyTyrGluProLeuIle 344
 Db 3391197 ACCATGACAAGGCCCTGGCCAGACGCGTCCCTGACGGA 3391250
 QY 345 ArgArgIle-----AspAlaPheArgAlaLeuTyrAsnAspT 357
 Db 3391251 GATCACGTTGCTGATCAGATCCTGGCGAAGACCTGCTCACCGTGTCCACGGACTGG 3391307

RESULT 10
 US-08-956-171E-324/c
 ; Sequence 324: Application US/08956171E

Patent No. 6593114
 GENERAL INFORMATION:
 APPLICANT: Charles Kunisch
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fanion
 TITLE OF INVENTION: staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5256
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: Windows version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/956-171E
 FILING DATE: 20-Oct-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/009,861
 FILING DATE: January 5, 1996
 APPLICATION NUMBER: 08/781,985
 FILING DATE: January 3, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Hyman
 REGISTRATION NUMBER: 46,789
 REFERENCE DOCKET NUMBER: PB248P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (240) 314-1224
 TELEFAX: (301) 309-8439
 INFORMATION FOR SEQ ID NO: 324:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5030 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 324:
 US-08-956-171E-324

Alignment Scores:
 Pred. No.: 0.0572 Length: 5030

Score: 103.00
 Percent Similarity: 38.62%
 Best Local Similarity: 21.17%
 Query Match: 4
 Db: 4

US-09-886-400A-4 (1-364) x US-08-956-171E-324 (1-5030)

QY 107 GluValSerProLygLygPheTrpLeuProGluLeuIleTyrAspProIleLeuProAla 126
 Db 2699 GAGATATCACCT-----TATTATGATTCATTA----- 2673
 QY 127 IleLeuIysAspAspGlyTyrGluLeuPheAlaAspGlyGluAlaMetLeuPheSer 146
 Db 2672 CTGPPAAATTATCTCACACCGGATATCATTACACGAGGAAATGGTACGC 2613
 QY 147 AlaHisLeuAsnSerAlaIleIysAspIleIysAspIleIysAspIleIysAla 166
 Db 2612 TCATTCAGAGAAATGGTATTCGTTGTTAAACTAATATTCCATTCTTAATTATGTA 2553
 QY 167 GluArgGluIysArgPhe-----ArgTyrIleSerTyrIleLeu 179
 Db 2552 ATGAAAGATAAAGACTCACAGTGTGATTAACACAATTAATTTCAGAGAACACCA 2493
 QY 180 GlyLeuArgGluLeuArgIle-----LysLeuValPheGluGly 194
 Db 2492 GAACTTCCGACATTCAGCGCTCTAGATAGAGGTACTAACATGATAGATATAGT 2433
 QY 195 LysValThrIleLeuIleAlaIleAspIleGlu----- 205
 Db 2432 ATGAAACATAATGGTCCCAAATGTTGAGAACGTCGAGAACAGACTATGATA 2373
 QY 206 --AlaValProValTrpValAlaValAsnThrValAlaMetLeuGlyIleGlyArg--- 223
 Db 2312 CTGATCAATCCAACTGTATCTCAAGTAAATCGCTCATTTAGTGACGAAATG 2313
 QY 224 LeuProLeuMetAsnProLybLysValAlaSerTrpIleGluAspIleLeu 243
 Db 2252 CTA-----ACAGATAACAACTTGGAGATGACACCAATCATTTAGCTACAGGTT 2199
 QY 263 SerValGluGlyLeuIleIysAspGluLeuSerGluLeuCysLeuProSer 282
 Db 2198 AGAACTAAGCATATGATTAATATCGATCC----- 219
 QY 283 GluIleIysHissArgGlyArgGluLeuIleTyrLeuArgThrSerSerTrpAlaProAspLys 302
 Db 2168 -----AAACAGGGAGCTTAAAGTGTG 2142
 QY 303 ---SerLeuArgIleTrpArgGluIlePheGluAsnAlaArgGluAsnMetLeuSerTyr 321
 Db 2141 TTCTTCACTAGAAATGCG-----GGCGGTGCTACATTGTATGTCGCTAT 2097
 QY 322 AspMetArgGlyGluLeuIlePheLeuAlaGluAsnSerAspAlaArgGlyTyrGluPro 341
 Db 2096 AAT-----TCTTGAAGGAACCCA-----TGGAAAGCA 2067
 QY 342 LeuProGluArgGluLeuAspAlaPheArgAlaLeuTyrAsn 355
 Db 2066 CTGAACTCTACGT-----AAGCTTCCAAAT 2037

RESULT 11
 US-08-781-986A-324/c
 ; Sequence 324: Application US/08781986A
 ; Patent No. 6737248
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunisch
 ; TITLE OF INVENTION: staphylococcus aureus Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 5256
 ; CORRESPONDENCE ADDRESS:

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